

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52, Search time 38.9691 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-1

Perfect score: 24
Sequence: 1 agtcgtacggagcagcataaat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*\n2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*\n3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*\n4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*\n5: /cgn2_6/prodata/1/ina/PCOTUS_COMB.seq:*\n6: /cgn2_6/prodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	945 3 US-08-816-977-1	Sequence 1, Appl
2	24	100.0	945 4 US-09-334-477-1	Sequence 1, Appl
3	24	100.0	969 3 US-08-816-977-20	Sequence 20, Appl
4	24	100.0	969 4 US-09-334-477-20	Sequence 20, Appl
5	24	100.0	981 3 US-08-816-977-36	Sequence 36, Appl
6	24	100.0	981 4 US-09-334-477-36	Sequence 36, Appl
7	24	100.0	1241 3 US-08-816-977-9	Sequence 9, Appl
8	24	100.0	1241 4 US-09-334-477-9	Sequence 9, Appl
9	24	100.0	2073 3 US-08-816-977-46	Sequence 46, Appl
10	24	100.0	2073 4 US-09-334-477-46	Sequence 46, Appl
11	24	100.0	2127 3 US-08-816-977-32	Sequence 32, Appl
12	24	100.0	2127 4 US-09-334-477-32	Sequence 32, Appl
13	24	100.0	48908 3 US-09-453-702B-137	Sequence 137, App
14	17.6	73.3	774 4 US-09-583-110-1639	Sequence 1639, App
15	17.2	71.7	150 4 US-08-979-847B-36	Sequence 36, Appl
16	17.2	71.7	297 1 US-08-471-724-2	Sequence 2, Appl
17	17.2	71.7	297 2 US-08-471-969-2	Sequence 2, Appl
18	17.2	71.7	297 2 US-08-384-137-2	Sequence 2, Appl
19	17.2	71.7	297 2 US-08-470-006A-2	Sequence 2, Appl
20	17.2	71.7	297 3 US-08-691-563C-2	Sequence 2, Appl
21	17.2	71.7	297 3 US-09-200-990-2	Sequence 2, Appl
22	17.2	71.7	297 3 US-09-133-411-2	Sequence 2, Appl
23	17.2	71.7	297 4 US-08-979-847B-2	Sequence 2, Appl
24	17.2	71.7	299 3 US-08-691-563C-40	Sequence 40, Appl
25	17.2	71.7	299 4 US-09-374-766-40	Sequence 40, Appl
26	17.2	71.7	1158 1 US-08-471-724-1	Sequence 1, Appl
27	17.2	71.7	1158 1 US-08-471-724-1	Sequence 1, Appl

C 28	17.2	71.7	1158 2 US-08-471-969-1	Sequence 1, Appl
C 29	17.2	71.7	1158 2 US-08-384-137-1	Sequence 1, Appl
C 30	17.2	71.7	1158 2 US-08-470-006A-1	Sequence 1, Appl
C 31	17.2	71.7	1158 3 US-08-691-563C-1	Sequence 1, Appl
C 32	17.2	71.7	1158 3 US-09-200-990-1	Sequence 1, Appl
C 33	17.2	71.7	1158 3 US-09-133-411-1	Sequence 1, Appl
C 34	17.2	71.7	1158 4 US-08-979-847B-1	Sequence 1, Appl
C 35	17.2	71.7	1158 4 US-08-979-847B-205	Sequence 205, App
C 36	17.2	71.7	1597 4 US-08-979-847B-205	Sequence 205, App
C 37	17.2	71.7	1600 4 US-08-979-847B-207	Sequence 207, App
C 38	17.2	71.7	1600 4 US-08-979-847B-207	Sequence 207, App
C 39	17.2	71.7	2304 4 US-08-979-847B-87	Sequence 87, Appl
C 40	17.2	71.7	2364 4 US-08-979-847B-88	Sequence 88, Appl
C 41	17.2	71.7	2391 4 US-08-691-563C-57	Sequence 57, Appl
C 42	17.2	71.7	2391 4 US-09-374-766-57	Sequence 57, Appl
C 43	17.2	71.7	2391 4 US-08-979-847B-53	Sequence 53, Appl
C 44	16.6	69.2	1230025 4 US-09-128-452A-1	Sequence 1, Appl
C 45	16	66.7	256 4 US-09-313-294A-938	Sequence 938, App

ALIGNMENTS

RESULT 1
US-08-816-977-1

Sequence 1, Application US/08816977

Patent No. 6080400

GENERAL INFORMATION:

APPLICANT: Williams, James A.

APPLICANT: Byrne, Lisa M.

APPLICANT: Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of

TITLE OF INVENTION: Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESSES:

ADDRESSER: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/816,977

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPMD-02450

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 945 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..945

US-08-816-977-1

Query Match

Best Local Similarity 100.0%; Score 24; DB 3; Length 945;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 7, 2005, 07:55:37 ; Search time 195.093 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-1
Perfect score: 24
Sequence: 1 agctgacggggatgcagataat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	39	US-10-085-056-28
2	24	100.0	502	US-10-425-821-93
3	24	100.0	879	US-10-765-580-9
4	24	100.0	945	US-09-334-477-1
5	24	100.0	969	US-09-334-477-20
6	24	100.0	981	US-09-334-477-36
7	24	100.0	1241	US-09-334-477-9
8	24	100.0	1507	US-10-765-580-11
9	24	100.0	2073	US-09-334-477-46
10	24	100.0	2127	US-09-334-477-32
11	24	100.0	48908	US-10-114-170-137
12	17.6	73.3	581	US-10-027-632-221193

13	17.6	73.3	581	US-10-027-632-221193	Sequence 221193, A
14	17.6	73.3	1414	US-10-369-493-36750	Sequence 36750, A
15	17.2	71.7	150	US-08-979-847-36	Sequence 36, App1
16	17.2	71.7	150	US-10-114-104-36	Sequence 36, App1
17	17.2	71.7	297	US-08-979-847-2	Sequence 2, App1
18	17.2	71.7	297	US-10-430-442-2	Sequence 2, App1
19	17.2	71.7	297	US-10-114-104-2	Sequence 2, App1
20	17.2	71.7	299	US-10-430-442-40	Sequence 40, App1
21	17.2	71.7	1158	US-08-979-847-1	Sequence 1, App1
22	17.2	71.7	1158	US-10-430-442-1	Sequence 1, App1
23	17.2	71.7	1158	US-10-114-104-1	Sequence 1, App1
24	17.2	71.7	1597	US-08-979-847-205	Sequence 205, App
25	17.2	71.7	1597	US-10-114-104-205	Sequence 205, App
26	17.2	71.7	1600	US-08-979-847-206	Sequence 206, App
27	17.2	71.7	1600	US-08-979-847-207	Sequence 206, App
28	17.2	71.7	1600	US-10-114-104-206	Sequence 207, App
29	17.2	71.7	1600	US-10-114-104-207	Sequence 87, App1
30	17.2	71.7	2304	US-08-979-847-87	Sequence 87, App1
31	17.2	71.7	2304	US-10-114-104-87	Sequence 88, App1
32	17.2	71.7	2365	US-08-979-847-88	Sequence 88, App1
33	17.2	71.7	2365	US-10-114-104-88	Sequence 53, App1
34	17.2	71.7	2391	US-08-979-847-53	Sequence 53, App1
35	17.2	71.7	2391	US-10-430-442-57	Sequence 87, App1
36	16.8	70.0	2391	US-10-114-104-53	Sequence 88, App1
37	16.8	70.0	1953	US-10-425-114-36262	Sequence 36262, A
38	16.8	70.0	1688	US-10-425-114-36459	Sequence 36459, A
39	16.8	70.0	3068	US-10-425-115-102745	Sequence 3598, Ap
40	16.8	70.0	3068	US-10-437-963-3598	Sequence 165722, A
41	16.6	69.2	456	US-10-027-632-40457	Sequence 40457, A
42	16.6	69.2	456	US-10-027-632-40457	Sequence 1040, Ap
43	16.6	69.2	525	US-09-728-444-1040	Sequence 35369, A
44	16.6	69.2	556	US-10-027-632-35369	
45	16.6	69.2	556	US-10-027-632-35369	

ALIGNMENTS

RESULT 1
US-10-085-056-28/c
Sequence 28, Application US/10085056
Publication No. US20030008305A1
GENERAL INFORMATION:
APPLICANT: MARUYAMA, TAKAHIRO
APPLICANT: ISHIGURO, TAKAHIRO
TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
FILE REFERENCE: 220081US0
CURRENT FILING DATE: 2002-05-30
PRIORITY APPLICATION NUMBER: JP 2001-58143
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-10-085-056-28

Query Match 100.0%; Score 24; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGACGGGGATGCAGATAAT 24
DB 29 AGCTGACGGGGATGCAGATAAT 6

RESULT 2
US-10-425-821-93

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 184.701 Seconds
(without alignments)
682,108 Million cell updates/sec

Title: US-10-089-487-2

Sequence: 1 ccgaccataagaagaactcat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: geneseq19808.*
2: geneseq19908.*
3: geneseq20008.*
4: geneseq20018.*
5: geneseq20028.*
6: geneseq20038.*
7: geneseq20048.*
8: geneseq20058.*
9: geneseq20068.*
10: geneseq20078.*
11: geneseq20088.*
12: geneseq20098.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	AAF61479	Aaf61479 EHRC huma
2	24	100.0	945	AAT42649	Aat42649 Verotoxig
3	24	100.0	945	AAAS1194	Aaas1194 E. coli v
4	24	100.0	945	ABK11775	Abk11775 E. coli v
5	24	100.0	969	AAT42663	Aat42663 Histidine
6	24	100.0	969	AAAS1208	Aaas1208 Recombina
7	24	100.0	969	ABK11789	Abk11789 CDNA enco
8	24	100.0	980	AAT42673	Aat42673 FLAG tag/
9	24	100.0	981	AAAS1218	Aaas1218 FLAG tag-
10	24	100.0	981	ABK11799	Abk11799 CDNA enco
11	24	100.0	1192	AAV11402	Aav11402 Shiga tox
12	24	100.0	1207	AAV11403	Aav11403 Shiga tox
13	24	100.0	1227	ADL25576	Adl25576 S. dysent
14	24	100.0	1227	ADL25577	Adl25577 S. sonnei
15	24	100.0	1227	ADL25578	Adl25578 Bacterioph
16	24	100.0	1230	AAQ12711	Aaq12711 Shiga-1ik
17	24	100.0	1230	AAT91637	Aat91637 Phage H19
18	24	100.0	1230	AAZ30662	Aaz30662 E. coli ba
19	24	100.0	1230	AAZ99018	Aaz99018 E. coli b
20	24	100.0	1235	AAV11404	Aav11404 Shiga tox
21	24	100.0	1241	AAT42653	Aat42653 Sequence

C 22	24	100.0	1241	3	AAAS1198	Aaas1198 DNA direc
C 23	24	100.0	1369	2	AAZ27687	Aaz27687 Verotoxin
C 24	24	100.0	1389	2	AAV11400	Aav11400 Shiga tox
C 25	24	100.0	2073	3	AAAS1226	Aaas1226 MBP-VT-1
C 26	24	100.0	2073	6	ABK11957	Abk11957 CDNA enco
C 27	24	100.0	2126	2	AAT42671	Aat42671 Maltose b
C 28	24	100.0	2127	3	AAAS1216	Aaas1216 MBP-VT-1
C 29	24	100.0	2127	6	ABK11797	Abk11797 CDNA enco
C 30	24	100.0	47879	10	ADCO0509	Adco0509 Enterohae
C 31	24	100.0	48908	9	ACD19124	Accl19124 E. coli 0
C 32	23.6	98.3	33	6	ABO87914	Abog87914 Enterohae
C 33	22.4	93.3	948	4	AAH01085	Aah01085 Escherich
C 34	22.4	93.3	1241	6	ABK11779	Abk11779 Polyclist
C 35	19	79.2	1072	2	AAT86332	Aat86332 BPI pepti
C 36	17.8	74.2	2155	10	ADBS2356	Adbs2356 Primary r
C 37	17.8	74.2	2155	10	ADL16217	Adl16217 Rat prote
C 38	17.8	74.2	134525	2	AAO04525	Aaog04525 Total bas
C 39	17.6	73.3	3633	8	ABT18908	Abt18908 Aspergill
C 40	17.6	73.3	3741	8	ABT20130	Abt20130 Aspergill
C 41	17.6	73.3	3741	8	ABT20728	Abt20728 Aspergill
C 42	17.6	73.3	3741	8	ABT18314	Abt18314 Aspergill
C 43	17.6	73.3	5741	8	ABT19534	Abt19534 Aspergill
C 44	17.6	73.3	5741	8	ABT17720	Abt17720 Aspergill
C 45	17.6	73.3	300000	10	ADBS6352	Adb6352 Human PTP

ALIGNMENTS

RESULT 1	AAF61479	standard; DNA; 24 BP.
ID	AAF61479	
XX	AAF61479;	
AC	18-JUN-2001	(first entry)
DT		
XX		
XX	EHRC human pathogen sexual PCR primer SEQ ID 2.	
DE		
XX	EHRC infection; multiplex amplification; detection; human; pig;	
KW	enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; ss.	
XX		
OS	Escherichia coli.	
XX		
XX	DE19946296-A1.	
XX		
PD	29-MAR-2001.	
XX		
PF	28-SEP-1999;	99DE-01046296.
XX		
PR	28-SEP-1999;	99DE-01046296.
XX		
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.	
XX		
XX	Gunzer F, Bellin T;	
PI		
XX	WPI, 2001-246145/26.	
DR		
XX	Primers for amplifying Shiga toxin sequences in Escherichia coli, useful	
PT	in multiplex amplification detection of enterohemorrhagic strains.	
XX		
PS	Claim 1; Page 10; 14pp; German.	
CC	This invention describes a novel primer (P1) which can be used in a	
CC	multiplex amplification reaction for detecting clinically important EHRC	
CC	(enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous	
XX	detection of human and pig pathogens in a single measurement	
SO	Sequence 24 BP; 10 A; 6 C; 5 G; 3 T; 0 U; 0 Other;	
Query Match	100.0%;	Score 24; DB 5; Length 24;
Best Local Similarity	100.0%;	Pred. No. 0.17;
Matches	24; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 195.093 seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-2

Perfect score: 24
Sequence: 1 ccggacacatagaagaactcat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	24	100.0	583 18	US-10-425-821-91 Sequence 91, Appl
C 2	24	100.0	879 17	US-10-765-580-9 Sequence 9, Appl
C 3	24	100.0	945 9	US-09-334-477-1 Sequence 1, Appl
C 4	24	100.0	969 9	US-09-334-477-20 Sequence 20, Appl
C 5	24	100.0	981 9	US-09-334-477-36 Sequence 36, Appl
C 6	24	100.0	1241 9	US-09-334-477-9 Sequence 9, Appl
C 7	24	100.0	1507 17	US-10-765-580-11 Sequence 11, Appl
C 8	24	100.0	2073 9	US-09-334-477-46 Sequence 46, Appl
C 9	24	100.0	2127 9	US-09-334-477-32 Sequence 32, Appl
C 10	24	100.0	48908 14	US-10-114-170-137 Sequence 137, Appl
C 11	23.6	98.3	33 17	US-10-250-997-13 Sequence 13, Appl
C 12	19	79.2	70 15	US-10-127-890-73 Sequence 73, Appl

13	19	79.2	78	15	US-10-127-890-74	Sequence 74, Appl
C 14	19	79.2	1072	9	US-09-765-527-250	Sequence 250, Appl
15	18.2	75.8	142947	18	US-10-719-993-6967	Sequence 6967, Appl
16	17.8	74.2	201	18	US-10-719-993-26595	Sequence 26595, Appl
C 17	17.8	74.2	2155	15	US-10-366-547-66	Sequence 47556, Appl
18	17.8	74.2	2155	15	US-10-366-547-66	Sequence 47556, Appl
C 19	17.8	74.2	33271	18	US-10-719-993-6996	Sequence 6996, Appl
20	17.8	74.2	786452	18	US-10-719-993-6996	Sequence 6996, Appl
21	17.6	73.3	1280	13	US-10-027-632-124418	Sequence 124418, Appl
22	17.6	73.3	1280	13	US-10-027-632-124418	Sequence 124418, Appl
23	17.6	73.3	3633	15	US-10-128-714-2078	Sequence 2078, Appl
24	17.6	73.3	3741	15	US-10-128-714-1078	Sequence 1078, Appl
25	17.6	73.3	3741	15	US-10-128-714-1078	Sequence 6078, Appl
26	17.6	73.3	3741	15	US-10-128-714-7078	Sequence 7078, Appl
27	17.6	73.3	5741	15	US-10-128-714-78	Sequence 78, Appl
28	17.6	73.3	5741	15	US-10-128-714-5078	Sequence 5078, Appl
C 29	17.6	73.3	107745	17	US-10-322-281-268	Sequence 268, Appl
C 30	17.6	73.3	300000	15	US-10-262-552-33	Sequence 33, Appl
C 31	17.6	73.3	300000	17	US-10-703-210-33	Sequence 33, Appl
C 32	17.4	72.5	1249	13	US-10-027-632-123375	Sequence 123375, Appl
C 33	17.4	72.5	1249	13	US-10-027-632-123375	Sequence 123375, Appl
C 34	17.4	72.5	1163020	16	US-10-398-221-10	Sequence 10, Appl
C 35	17.4	72.5	3011208	16	US-10-398-221-2058	Sequence 2058, Appl
36	17.2	71.7	230	15	US-10-106-698-2194	Sequence 2194, Appl
C 37	17.2	71.7	370	18	US-10-425-115-55577	Sequence 55577, Appl
38	17.2	71.7	620	17	US-10-437-963-39794	Sequence 39794, Appl
C 39	17.2	71.7	758	15	US-10-012-697-1050	Sequence 1050, Appl
40	17.2	71.7	2484	15	US-10-325-881-68	Sequence 68, Appl
C 41	17.2	71.7	2679	15	US-10-369-493-40501	Sequence 40501, Appl
42	17.2	71.7	2859	15	US-10-094-749-1325	Sequence 1325, Appl
C 43	17.2	71.7	7734	9	US-09-764-868-1317	Sequence 1317, Appl
44	17.2	71.7	21184	15	US-10-017-161-703	Sequence 703, Appl
45	17.2	71.7	48459	13	US-10-087-192-424	Sequence 424, Appl

ALIGNMENTS

RESULT 1
US-10-425-821-91/c
; Sequence 91, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos,e
; APPLICANT: BERKAL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425, 821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-91

Query Match 100.0%; Score 24; DB 18; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0

QY 1 CCGACACATAGAGAACTCAT 24
DB 247 CCGACACATAGAGAACTCAT 224

RESULT 2
US-10-765-580-9/c
; Sequence 9, Application US/10765580
; Publication No. US2004016565A1
; GENERAL INFORMATION:
; APPLICANT: Backer, Martina V.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 153.918 Seconds

(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-3

Sequence: 1 ttccggaatgcacatcagtc 20

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gapext 1.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_238ep04:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AA61480	Aa61480 EHEC pig
2	20	100.0	34	ABX94717	ABX94717 EHEC ST12
3	20	100.0	282	ADN02038	ADN02038 Enterohae
4	20	100.0	540	AA05942	Aa05942 Genomic D
5	20	100.0	540	AA21896	Aa21896 E. coli O
6	20	100.0	954	AA42651	Aa42651 Verotoxin
7	20	100.0	954	AA51196	Aa51196 E. coli V
8	20	100.0	954	ABK11777	ABK11777 E. coli V
9	20	100.0	960	ADH34345	ADH34345 Verotoxin
10	20	100.0	960	ADH34301	ADH34301 Verotoxin
11	20	100.0	960	ADH34343	ADH34343 Verotoxin
12	20	100.0	960	ADH34339	ADH34339 Verotoxin
13	20	100.0	960	ADH34337	ADH34337 Verotoxin
14	20	100.0	960	ADH34341	ADH34341 Verotoxin
15	20	100.0	960	ADH34335	ADH34335 Verotoxin
16	20	100.0	980	AA74265	Aa74265 Histidine
17	20	100.0	981	AA51210	Aa51210 Recombina
18	20	100.0	981	ABK11791	ABK11791 CDNA enco
19	20	100.0	989	AA742674	Aa742674 Flag tag/
20	20	100.0	990	AA51219	Aa51219 FLAG tag-
21	20	100.0	990	ABK11800	ABK11800 CDNA enco

22	20	100.0	1201	2	AAV11405	AAV11405 Shiga tox
23	20	100.0	1217	2	AAV11406	AAV11406 Shiga tox
24	20	100.0	1232	11	ADL25585	ADL25585 E. cloacae
25	20	100.0	1232	11	ADL25580	ADL25580 E. coli s
26	20	100.0	1232	11	ADL25578	ADL25578 E. coli s
27	20	100.0	1234	11	ADL25582	ADL25582 E. coli s
28	20	100.0	1234	11	ADL25581	ADL25581 E. coli s
29	20	100.0	1235	2	AA742654	Aa742654 Sequence
30	20	100.0	1235	6	AA51199	Aa51199 DNA direc
31	20	100.0	1235	6	ABK11780	ABK11780 Polyclstr
32	20	100.0	1235	11	ADL25584	ADL25584 E. coli s
33	20	100.0	1235	11	ADL25583	ADL25583 E. coli s
34	20	100.0	1242	3	AA244676	Aa244676 E. coli s
35	20	100.0	1254	4	AA227653	Aa227653 E. coli s
36	20	100.0	1254	10	ADH22653	ADH22653 Escherich
37	20	100.0	1259	2	AAH01086	AaH01086 Escherich
38	20	100.0	1479	4	AAV11401	AAV11401 Shiga tox
39	20	100.0	1612	8	ACA64707	ACA64707 Verotoxin
40	20	100.0	1612	10	ADP43307	ADP43307 Superant
41	20	100.0	1664	2	AA227668	Aa227668 Verotoxin
42	20	100.0	2085	6	AA51227	Aa51227 MBP-VT-2
43	20	100.0	2085	6	ABK11958	ABK11958 CDNA enco
44	20	100.0	2135	2	AA742672	Aa742672 Maltose b
45	20	100.0	2136	3	AA51217	Aa51217 MBP-VT-2

ALIGNMENTS

RESULT 1
AA61480
ID AAF61480 standard; DNA; 20 BP.

AC AAF61480;

DT 18-JUN-2001 (first entry)

DE EHEC pig pathogen strxA2 PCR primer SEQ ID 3.

DX EHEC infection; multiplex amplification; detection; human; pig;

KW enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; ss.

XX Escherichia coli.

OS DE1946296-A1.

PN 29-MAR-2001.

PD 28-SEP-1999; 99DE-01046296.

PF 28-SEP-1999; 99DE-01046296.

PR 28-SEP-1999; 99DE-01046296.

PS (HOFF) ROCHE DIAGNOSTICS GMBH.

PI Gunzer F, Bellin T;

XX WPI, 2001-246145/26.

XX Primers for amplifying Shiga toxin sequences in Escherichia coli, useful

XX in multiplex amplification detection of enterohemorrhagic strains.

XX Claim 1, Page 10, 14pp; German.

XX This invention describes a novel primer (P1) which can be used in a

XX multiplex amplification reaction for detecting clinically important EHEC

XX (enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous

XX detection of human and pig pathogens in a single measurement

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 5; Length 20;

XX Best local similarity 100.0%; Pred. No. 1.8;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 32.4742 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-3

Sequence: 1 ttccggaatgcataatcagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	540	3	US-09-147-251-1
2	20	100.0	954	3	US-08-816-977-5
3	20	100.0	954	4	US-09-334-477-5
4	20	100.0	981	3	US-08-816-977-24
5	20	100.0	981	4	US-09-334-477-24
6	20	100.0	990	3	US-08-816-977-38
7	20	100.0	990	4	US-09-334-477-38
8	20	100.0	1235	3	US-08-816-977-10
9	20	100.0	1235	4	US-09-334-477-10
10	20	100.0	1235	4	US-09-599-032A-3
11	20	100.0	2085	3	US-08-816-977-48
12	20	100.0	2085	4	US-09-334-477-48
13	20	100.0	2136	3	US-08-816-977-34
14	20	100.0	2136	4	US-09-334-477-34
15	20	100.0	61663	3	US-09-453-7028-62
16	15.8	79.0	1664976	4	US-08-916-421B-1
17	15.8	79.0	1664976	4	US-09-692-570-1
18	15.4	77.0	240	4	US-09-489-039A-1762
19	15.4	77.0	636	4	US-09-270-767-2119
20	15.4	77.0	636	4	US-09-270-767-17401
21	15.2	76.0	252	3	US-08-905-223-245
22	15.2	76.0	2035	4	US-08-849-602-12
23	15.2	76.0	2273	2	US-08-788-539A-1
24	15.2	76.0	3343	3	US-08-965-762-19
25	15.2	76.0	3343	4	US-09-911-927-19
26	15.2	76.0	3343	4	US-09-911-927-21
27	15.2	76.0	3343	4	US-09-911-882-19

28	15.2	76.0	3343	4	US-09-911-882-21	Sequence 21, Appl
29	15.2	76.0	3343	4	US-09-911-888-19	Sequence 19, Appl
30	15.2	76.0	3343	4	US-09-911-888-21	Sequence 21, Appl
31	15.2	76.0	4164	1	US-08-188-582-3	Sequence 3, Appl
32	15.2	76.0	4164	1	US-08-646-715-3	Sequence 1099, Appl
33	15.2	76.0	18431	4	US-09-221-017B-1090	Sequence 3, Appl
34	15.2	76.0	41	3	US-09-289-751-3	Sequence 34730, A
35	14.8	74.0	385	4	US-09-513-999C-34730	Sequence 11546, A
36	14.8	74.0	1098	4	US-09-270-767-11546	Sequence 2372, Ap
37	14.8	74.0	1272	4	US-09-248-796A-2372	Sequence 2376, Ap
38	14.8	74.0	1386	4	US-09-248-796A-2376	Sequence 13, Appl
39	14.8	74.0	4953	4	US-09-602-787A-13	Sequence 55, Appl
40	14.8	74.0	4953	4	US-09-602-787A-55	Sequence 3, Appl
41	14.8	74.0	99916	4	US-09-816-095-3	Sequence 34730, A
42	14.4	72.0	32	4	US-09-828-303-34	Sequence 34, Appl
43	14.4	72.0	354	4	US-09-513-999C-34934	Sequence 34934, A
44	14.4	72.0	3001	4	US-09-539-333D-214	Sequence 214, App
45	14.4	72.0	41100	4	US-09-755-655-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-147-251-1
Sequence 1, Application US/09147251
Patent No. 6391546
GENERAL INFORMATION:
APPLICANT: KARUBE, Isao
APPLICANT: SAMATA, Shinya
APPLICANT: NAGATA, Ryohel
TITLE OF INVENTION: METHOD FOR DETECTING TARGET NUCLEOTIDE SEQUENCE
FILE REFERENCE: 7867-0002-0XPCT
CURRENT APPLICATION NUMBER: US/09/147,251
CURRENT FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: JP117735/1997
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: JP74442/1998
EARLIER FILING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP123371/1998
EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 540
TYPE: DNA
ORGANISM: Escherichia coli
US-09-147-251-1

Query Match 100.0%; Score 20; DB 3; Length 540;
Best local similarity 100.0%; Pred. No. 0.22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGAATGCATAATCAGTC 20
DB 441 TTCCGGAATGCATAATCAGTC 460

RESULT 2
US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 162.577 Seconds
(without alignments) 706.850 Million cell updates/sec

Title: US-10-089-487-3
Perfect score: 20
Sequence: 1 ttccggaatgcaatcagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	482	18	US-10-425-821-94
2	20	100.0	540	14	US-10-103-798-1
3	20	100.0	540	15	US-10-334-831-1
4	20	100.0	954	9	US-09-334-477-5
5	20	100.0	981	9	US-09-334-477-24
6	20	100.0	990	9	US-09-334-477-38
7	20	100.0	1235	9	US-09-334-477-10
8	20	100.0	1612	10	US-09-870-759-27
9	20	100.0	1612	10	US-09-751-708A-27
10	20	100.0	1612	18	US-10-428-817A-23
11	20	100.0	1612	18	US-10-425-821-92
12	20	100.0	2085	9	US-09-334-477-48

13	20	100.0	2136	9	US-09-334-477-34	Sequence 34, Appl
14	20	100.0	61662	14	US-10-418-837-1	Sequence 1, Appl
15	20	100.0	61663	16	US-10-114-170-62	Sequence 62, Appl
16	16.8	84.0	4689	16	US-10-282-122A-33564	Sequence 33564, A
17	16.8	84.0	5855	18	US-10-783-528-52	Sequence 52, Appl
18	16.8	84.0	38234	13	US-10-087-192-1762	Sequence 1762, Ap
19	16.4	82.0	810	15	US-10-369-499-32514	Sequence 32514, A
20	15.8	79.0	704	18	US-10-653-047-5739	Sequence 5739, Ap
21	15.8	79.0	1080	15	US-10-369-493-41357	Sequence 41357, A
22	15.8	79.0	1536	18	US-10-425-115-25113	Sequence 25113, A
23	15.8	79.0	2303	17	US-10-767-701-13781	Sequence 13781, A
24	15.8	79.0	2303	18	US-10-425-115-23429	Sequence 23429, A
25	15.8	79.0	173808	13	US-10-003-806-10	Sequence 10, Appl
26	15.4	77.0	201	16	US-10-282-122A-19911	Sequence 19911, A
27	15.4	77.0	201	16	US-10-282-122A-23805	Sequence 23805, A
28	15.4	77.0	361	17	US-10-767-701-27245	Sequence 27245, A
29	15.4	77.0	494	13	US-10-027-632-311865	Sequence 311865, A
30	15.4	77.0	494	15	US-10-027-632-311865	Sequence 311865, A
31	15.4	77.0	497	13	US-10-027-632-57834	Sequence 57834, A
32	15.4	77.0	497	13	US-10-027-632-57834	Sequence 57834, A
33	15.4	77.0	612	13	US-10-027-632-5921	Sequence 5921, Ap
34	15.4	77.0	612	15	US-10-027-632-5921	Sequence 5921, Ap
35	15.4	77.0	3063	16	US-10-424-599-106545	Sequence 106545, A
36	15.4	77.0	3575	16	US-10-424-599-106545	Sequence 106545, A
37	15.2	76.0	180	14	US-10-198-846-10248	Sequence 10248, A
38	15.2	76.0	359	9	US-09-864-761-24185	Sequence 24185, A
39	15.2	76.0	375	18	US-10-425-115-39740	Sequence 39740, A
40	15.2	76.0	473	10	US-09-918-995-2619	Sequence 2619, Ap
41	15.2	76.0	476	14	US-10-198-846-63	Sequence 63, Appl
42	15.2	76.0	558	9	US-09-864-761-7471	Sequence 7471, Appl
43	15.2	76.0	559	17	US-10-767-701-16023	Sequence 16023, A
44	15.2	76.0	562	16	US-10-259-194A-526	Sequence 526, Appl
45	15.2	76.0	567	18	US-10-357-930-60418	Sequence 60418, A

ALIGNMENTS

RESULT 1
US-10-425-821-94 Application US/10425821
Publication NO. US20040219530A1
GENERAL INFORMATION:
APPLICANT: BROUSSEAU, Roland
APPLICANT: HAREL, Jos'e
APPLICANT: BEKAL, Sad'ia
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCES: 86369-3
CURRENT APPLICATION NUMBER: US/10/425,821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn version 3.2
SEQ ID NO 94
LENGTH: 482
TYPE: DNA
ORGANISM: Escherichia coli
US-10-425-821-94

Query Match 100.0%; Score 20; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGAATGCAATCAGTC 20
DB 294 TTCCGGAATGCAATCAGTC 313

RESULT 2
US-10-103-798-1
Publication US/10103798
Publication NO. US20030054378A1
GENERAL INFORMATION:
APPLICANT: KARUBE, Isao

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 161.613 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21

Sequence: 1 cgatactccggaagacatcg 21

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	5	AAF61481
2	21	100.0	954	2	AAT42651
3	21	100.0	954	3	AAAS1196
4	21	100.0	954	6	ABK11777
5	21	100.0	960	10	ADH34345
6	21	100.0	960	10	ADH34301
7	21	100.0	960	10	ADH34339
8	21	100.0	960	10	ADH34337
9	21	100.0	960	10	ADH34341
10	21	100.0	960	10	ADH34335
11	21	100.0	980	2	AAT42665
12	21	100.0	981	6	ABK11791
13	21	100.0	989	2	AAT42674
14	21	100.0	990	3	AAAS1219
15	21	100.0	990	6	ABK11800
16	21	100.0	1201	2	AAV11405
17	21	100.0	1217	2	AAV11406
18	21	100.0	1232	11	ADL25585
19	21	100.0	1232	11	ADL25580
20	21	100.0	1232	11	ADL25580
21	21	100.0	1232	11	ADL25580

C 22	21	100.0	1232	11	ADL25578	AdL25578 E. coli s
C 23	21	100.0	1235	2	AAT42654	Aat42654 Sequence
C 24	21	100.0	1235	3	AAAS1199	AAAS1199 DNA direc
C 25	21	100.0	1235	6	ABK11780	ABK11780 Polyclatr
C 26	21	100.0	1235	11	ADL25584	AdL25584 E. coli s
C 27	21	100.0	1235	11	ADL25583	AdL25583 E. coli s
C 28	21	100.0	1242	3	AAZ44676	Aaz44676 E. coli s
C 29	21	100.0	1254	4	ACG91779	Acg91779 Escherich
C 30	21	100.0	1254	10	ADH22653	Adh22653 Escherich
C 31	21	100.0	1259	4	AAH01086	Aah01086 Escherich
C 32	21	100.0	1479	2	AAV11401	Aav11401 Shiga tox
C 33	21	100.0	1612	8	ACA64707	AcA64707 Verotoxin
C 34	21	100.0	1612	10	ADP43307	AdP43307 Superant
C 35	21	100.0	1664	2	AAZ27688	Aaz27688 Verotoxin
C 36	21	100.0	2085	3	AAAS1227	AAAS1227 MBP-VT-2
C 37	21	100.0	2085	6	ABK11958	Abk11958 CDNA enco
C 38	21	100.0	2135	2	AAT42672	Aat42672 Maltose b
C 39	21	100.0	2136	3	AAAS1217	AaAS1217 MBP-VT-2
C 40	21	100.0	2136	6	ABK11798	Abk11798 CDNA enco
C 41	21	100.0	61663	9	ACD19049	Adc19049 E. coli 0
C 42	21	100.0	62708	10	ADC00199	Adc00199 Enterohae
C 43	21	100.0	134141	6	ABN83487	Abn83487 Escherich
C 44	19.4	92.4	1234	11	ADL25582	AdL25582 E. coli s
C 45	19.4	92.4	1234	11	ADL25581	AdL25581 E. coli s

ALIGNMENTS

RESULT 1
AAF61481
ID AAF61481 standard; DNA: 21 BP.
AC AAF61481;
DT 18-JUN-2001 (first entry)
XX
DE EHEC pig pathogen stx2 PCR primer SEQ ID 4.
XX
KW EHEC infection; multiplex amplification; detection; human; pig;
XX enterohemorrhagic Escherichia coli infection; pathogen; PCR primer; se.
XX
OS Escherichia coli.
XX
PN DE19946296-A1.
XX
PD 29-MAR-2001.
XX
PF 28-SEP-1999; 99DE-01046296.
XX
PR 28-SEP-1999; 99DE-01046296.
XX
PA (HOF) ROCHER DIAGNOSTICS GMBH.
XX
PI Gunzer F, Bellin T;
XX
XX WPI; 2001-246145/26.
XX
PT Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
XX in multiplex amplification detection of enterohemorrhagic strains.
XX
PS Claim 1; Page 10; 14pp; German.
XX
CC This invention describes a novel primer (PI) which can be used in a
XX multiplex amplification reaction for detecting clinically important EHEC
CC (enterohemorrhagic Escherichia coli) infections. PI allow simultaneous
XX detection of human and pig pathogens in a single measurement
SQ Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 34.0979 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21
Sequence: 1 cgaataccggaagacacatg 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
C 1	21	100.0	954	3	US-08-816-977-5
C 2	21	100.0	954	4	US-09-334-477-5
C 3	21	100.0	981	3	US-08-816-977-24
C 4	21	100.0	981	4	US-09-334-477-24
C 5	21	100.0	980	3	US-08-816-977-38
C 6	21	100.0	990	4	US-09-334-477-38
C 7	21	100.0	1235	3	US-08-816-977-10
C 8	21	100.0	1235	4	US-09-334-477-10
C 9	21	100.0	1254	4	US-09-599-032A-3
C 10	21	100.0	2085	4	US-08-816-977-48
C 11	21	100.0	2085	4	US-09-334-477-48
C 12	21	100.0	2136	3	US-08-816-977-34
C 13	21	100.0	2136	4	US-09-334-477-34
C 14	21	100.0	61663	3	US-09-453-702B-62
C 15	15.8	75.2	4672	4	US-09-221-017B-846
C 16	15.4	73.3	366	4	US-08-956-171E-4332
C 17	15.4	73.3	366	4	US-08-781-986A-4332
C 18	15.4	73.3	2933	3	US-08-936-165A-201
C 19	15.4	73.3	4330	3	US-09-310-293-1
C 20	15.4	73.3	4330	3	US-09-579-376-1
C 21	15.4	73.3	14051	4	US-08-956-171E-103
C 22	15.4	73.3	14051	4	US-08-781-986A-103
C 23	15.2	72.4	302	4	US-09-726-457-1002
C 24	15.2	72.4	302	4	US-09-736-457-1002
C 25	15.2	72.4	302	4	US-09-614-124B-1002
C 26	15.2	72.4	302	4	US-09-671-325-1002
C 27	15.2	72.4	302	4	US-09-658-824-1002

C 28	15.2	72.4	465	4	US-09-248-796A-3824	Sequence 3824, Ap
C 29	15.2	72.4	555	4	US-09-727-769A-5	Sequence 5, Appl
C 30	15.2	72.4	591	4	US-09-540-236-742	Sequence 742, Appl
C 31	15.2	72.4	799	3	US-08-998-416-424	Sequence 424, App
C 32	15.2	72.4	973	4	US-09-270-767-10330	Sequence 10330, A
C 33	15.2	72.4	1080	4	US-09-727-769A-7	Sequence 7, Appl
C 34	15.2	72.4	1188	4	US-09-362-843-5	Sequence 5, Appl
C 35	15.2	72.4	2121	4	US-09-489-039A-5009	Sequence 5009, Ap
C 36	15.2	72.4	3348	3	US-09-302-620B-94	Sequence 94, Appl
C 37	15.2	72.4	3348	3	US-09-912-161-12	Sequence 12, Appl
C 38	15.2	72.4	5060	2	US-08-656-555-2	Sequence 2, Appl
C 39	15.2	72.4	5062	2	US-08-656-555-1	Sequence 1, Appl
C 40	15.2	72.4	66986	4	US-09-596-002-29	Sequence 29, Appl
C 41	15.2	72.4	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C 42	14.8	70.5	81	1	US-08-238-863-84	Sequence 84, Appl
C 43	14.8	70.5	81	1	US-08-443-407-84	Sequence 84, Appl
C 44	14.8	70.5	81	5	PCT-US95-05600-228	Sequence 228, App
C 45	14.8	70.5	327	4	US-09-270-767-305	Sequence 305, App

ALIGNMENTS

RESULT 1
US-08-816-977-5/c
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSES: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 21; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 230.876 Seconds

(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-5

Perfect score: 30

Sequence: 1 ctgtcacagracacaaccgtacatgcctc 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003s:*
7: geneseq2004s:*
8: geneseq2005s:*
9: geneseq2006s:*
10: geneseq2007s:*
11: geneseq2008s:*
12: geneseq2009s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	AA61482	AA61482 EHRC huma
2	30	100.0	287	ADN02037	Adn02037 Enterohae
3	30	100.0	870	ADL14887	Adl14887 DNA encod
4	30	100.0	945	AA742649	Aa742649 Verotoxig
5	30	100.0	945	AA51194	Aa51194 E. coli v
6	30	100.0	945	AA511775	Abk11775 E. coli v
7	30	100.0	948	AAH01085	AaH01085 Escherich
8	30	100.0	969	AA742663	Aa742663 Histidine
9	30	100.0	969	AA51208	Aa51208 Recombina
10	30	100.0	969	ABK11789	Abk11789 CDNA enco
11	30	100.0	980	AA742673	Aa742673 FLAG tag/
12	30	100.0	981	AA51218	Abk11799 CDNA enco
13	30	100.0	1192	AAV11402	AaV11402 Shiga tox
14	30	100.0	1207	AAV11403	AaV11403 Shiga tox
15	30	100.0	1227	ADL25576	Adl25576 S. dysent
16	30	100.0	1227	ADL25577	Adl25577 S. sonnei
17	30	100.0	1227	AA012711	Aa012711 Shiga-11k
18	30	100.0	1230	AA012711	Aa012711 Shiga-11k
19	30	100.0	1230	AA791637	Aa791637 Phage H19
20	30	100.0	1230	AA791637	Aa791637 Phage H19
21	30	100.0	1230	AA730662	Aa730662 E. coli ba

C 22	30	100.0	1230	3	AA290018	Aa290018 E. coli b
C 23	30	100.0	1235	2	AAV11404	AaV11404 Shiga tox
C 24	30	100.0	1241	2	AA742653	Aa742653 Sequence
C 25	30	100.0	1241	3	AA51198	Aa51198 DNA direc
C 26	30	100.0	1241	6	ABK11779	Abk11779 Polycistr
C 27	30	100.0	1369	2	AA227687	Aa227687 Verotoxin
C 28	30	100.0	1389	2	AAV11400	AaV11400 Shiga tox
C 29	30	100.0	2073	3	AA51226	Aa51226 MBP-VT-1
C 30	30	100.0	2073	6	ABK11957	Abk11957 CDNA enco
C 31	30	100.0	2126	2	AA742671	Aa742671 Maltose b
C 32	30	100.0	2127	3	AA51216	Aa51216 MBP-VT-1
C 33	30	100.0	2127	6	ABK11797	Abk11797 CDNA enco
C 34	30	100.0	47879	10	ADCC0509	Adc0509 Enterohae
C 35	30	100.0	48908	9	ADC19124	Adc19124 E. coli o
C 36	20.4	68.0	4384	10	AD562393	Ad562393 Rat gene
C 37	20.4	68.0	4384	10	AD562393	Ad562393 Rat gene
C 38	20	65.7	280	6	ABL70886	AbL70886 Corn tase
C 39	19.6	65.3	349980	6	ABQ81845	AbQ81845 Bifidobac
C 40	19.4	64.7	1046	4	AA76385	Aa76385 T. harzia
C 41	19.4	64.7	2256	4	AA76385	Aa76385 T. harzia
C 42	18.8	62.7	612	5	AAH81342	AaH81342 Escherich
C 43	18.8	62.7	996	5	AA592716	Aa592716 DNA encod
C 44	18.8	62.7	1235	11	ADL25579	Adl25579 E. coli s
C 45	18.6	62.0	282	6	ABN22472	Abn22472 Human ORF

ALIGNMENTS

RESULT 1
AA61482
ID AA61482 standard; DNA; 30 BP.

XX AA61482;

DT 18-JUN-2001 (first entry)

DE EHRC human pathogen stx1 probe SEQ ID 5.

KW EHRC infection; multiplex amplification; detection; human; pig;

KW enterohemorrhagic Escherichia coli infection; pathogen; probe; ss.

XX Escherichia coli.

OS DE19946296-A1.

XX 29-MAR-2001.

XX 28-SEP-1999; 99DE-01046296.

XX 28-SEP-1999; 99DE-01046296.

XX 28-SEP-1999; 99DE-01046296.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PI Gunzer F, Bellin T;

DR WPI, 2001-246145/26.

PT Primers for amplifying Shiga toxin sequences in Escherichia coli; useful

PT in multiplex amplification detection of enterohemorrhagic strains.

XX Claim 11; Page 10; 14pp; German.

PS This invention describes a novel primer (P1) which can be used in a

CC multiplex amplification reaction for detecting clinically important EHRC

CC (enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous

CC detection of human and pig pathogens in a single measurement

XX Sequence 30 BP; 10 A; 10 C; 4 G; 6 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 30; DB 5; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gencore version 5.1.6
Copyright (c) 1993 - 2005 Compygen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 48.7113 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-5

Perfect score: 30

Sequence: 1 ccgtcacgtacacacgcgtacatgcgc 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCUTS_COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	945	3	US-08-816-977-1
2	30	100.0	945	4	US-09-334-477-1
3	30	100.0	945	3	US-08-816-977-20
4	30	100.0	945	4	US-09-334-477-20
5	30	100.0	945	3	US-08-816-977-36
6	30	100.0	945	4	US-09-334-477-36
7	30	100.0	945	3	US-08-816-977-9
8	30	100.0	945	4	US-09-334-477-9
9	30	100.0	945	3	US-08-816-977-46
10	30	100.0	945	4	US-09-334-477-46
11	30	100.0	945	3	US-08-816-977-32
12	30	100.0	945	4	US-09-334-477-32
13	30	100.0	945	3	US-08-816-977-137
14	30	100.0	945	4	US-09-334-477-137
15	30	100.0	945	3	US-08-816-977-1
16	30	100.0	945	4	US-09-334-477-1
17	30	100.0	945	3	US-08-816-977-20
18	30	100.0	945	4	US-09-334-477-20
19	30	100.0	945	3	US-08-816-977-36
20	30	100.0	945	4	US-09-334-477-36
21	30	100.0	945	3	US-08-816-977-9
22	30	100.0	945	4	US-09-334-477-9
23	30	100.0	945	3	US-08-816-977-46
24	30	100.0	945	4	US-09-334-477-46
25	30	100.0	945	3	US-08-816-977-32
26	30	100.0	945	4	US-09-334-477-32
27	30	100.0	945	3	US-08-816-977-137

28	17.2	57.3	1235	3	US-08-816-977-10	Sequence 10, Appl
29	17.2	57.3	1235	4	US-09-334-477-10	Sequence 10, Appl
30	17.2	57.3	1254	4	US-09-599-032A-3	Sequence 3, Appl
31	17.2	57.3	1644	4	US-09-248-796A-3594	Sequence 3594, Ap
32	17.2	57.3	2085	3	US-08-816-977-48	Sequence 48, Appl
33	17.2	57.3	2085	4	US-09-334-477-48	Sequence 48, Appl
34	17.2	57.3	2136	3	US-08-816-977-34	Sequence 34, Appl
35	17.2	57.3	2136	4	US-09-334-477-34	Sequence 34, Appl
36	17.2	57.3	3678	4	US-09-112-580-13	Sequence 13, Appl
37	17.2	57.3	50341	1	US-08-247-901C-1	Sequence 1, Appl
38	17.2	57.3	50341	2	US-09-075-904-1	Sequence 1, Appl
39	17.2	57.3	52297	3	US-09-426-436-1	Sequence 1, Appl
40	17.2	57.3	52297	3	US-08-705-557-1	Sequence 1, Appl
41	17.2	57.3	61663	3	US-09-453-702B-62	Sequence 62, Appl
42	17.2	57.3	246240	2	US-08-724-394A-20	Sequence 20, Appl
43	17.2	57.3	246240	2	US-08-724-394A-21	Sequence 21, Appl
44	17.2	57.3	246240	2	US-08-724-394A-22	Sequence 22, Appl
45	17.2	56.7	765	4	US-09-543-681A-919	Sequence 919, App

ALIGNMENTS

RESULT 1
US-08-816-977-1/C
Sequence 1, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M. S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPMD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..945
US-08-816-977-1
Query Match 100.0%; Score 30; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGW note: this result is a transfer of the original file

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

Search, using sw model

February 7, 2005, 07:55:37, Search time 243.866 Seconds
(without alignments)
706.850 Million cell updates/sec

US-10-089-487-5

Perfected score: 30
Sequence: 1 ctgtcaccagtaacaacgcgtacatcgctc 30

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	30	100.0	502	18	US-10-425-821-93
2	30	100.0	879	17	US-10-765-580-9
3	30	100.0	945	9	US-09-334-477-1
4	30	100.0	969	9	US-09-334-477-20
5	30	100.0	961	9	US-09-334-477-36
6	30	100.0	1241	9	US-09-334-477-9
7	30	100.0	1507	17	US-10-765-580-11
8	30	100.0	2073	9	US-09-334-477-46
9	30	100.0	2137	9	US-09-334-477-32
10	30	100.0	48908	14	US-10-114-170-137
11	20	66.7	280	9	US-09-294-0938-260
12	20	66.7	284	18	US-10-425-115-152542

13	19.6	65.3	2256646	17	US-10-470-565-1	Sequence 1, Appli
14	19.4	64.7	542	18	US-10-425-115-67603	Sequence 67603, A
15	19.4	64.7	589	17	US-10-767-701-580	Sequence 580, App
16	19	63.3	867	17	US-10-437-963-102333	Sequence 102333,
17	19	63.3	1377	17	US-10-437-963-102335	Sequence 102335,
18	18.8	62.7	612	9	US-09-741-669-141	Sequence 141, App
19	18.8	62.7	1171	18	US-10-425-115-69448	Sequence 69448, A
20	18.8	62.7	1263	17	US-10-437-963-33404	Sequence 33404, A
21	18.8	62.7	3609	17	US-10-437-963-52742	Sequence 52742, A
22	18.8	62.7	253861	17	US-10-741-601-5611	Sequence 5611, Ap
23	18.8	62.7	261817	13	US-10-087-192-2002	Sequence 2002, Ap
24	18.6	62.0	604	13	US-10-027-632-164	Sequence 164, App
25	18.6	62.0	604	15	US-10-027-632-164	Sequence 164, App
26	18.6	62.0	612	16	US-10-260-238-4520	Sequence 4520, Ap
27	18.6	62.0	717	16	US-10-282-1224-22378	Sequence 22378, A
28	18.6	62.0	858	18	US-10-425-115-7917	Sequence 7917, Ap
29	18.6	62.0	864	18	US-10-425-115-7915	Sequence 7915, Ap
30	18.6	62.0	1199	16	US-10-260-238-4370	Sequence 4370, Ap
31	18.6	62.0	27150	17	US-10-697-828-20	Sequence 20, Appl
32	18.6	62.0	1830121	14	US-10-329-960-1	Sequence 1, Appli
33	18.6	62.0	1830121	16	US-10-329-970-1	Sequence 1, Appli
34	18.6	62.0	1830121	18	US-10-158-865-1	Sequence 190542,
35	18.4	61.3	572	13	US-10-027-632-190542	Sequence 190542,
36	18.4	61.3	572	15	US-10-027-632-190542	Sequence 229, App
37	18.2	60.7	650	10	US-09-854-867-229	Sequence 11641, A
38	18.2	60.7	941	18	US-10-363-345A-11641	Sequence 11642, A
39	18.2	60.7	941	18	US-10-363-345A-11642	Sequence 91, Appl
40	18.2	60.7	1554	15	US-09-533-029-91	Sequence 29, Appl
41	18.2	60.7	1554	15	US-10-278-536-29	Sequence 1103, Ap
42	18.2	60.7	1554	15	US-10-225-066A-1103	Sequence 109, App
43	18.2	60.7	1554	16	US-10-374-780A-109	Sequence 361, App
44	18.2	60.7	1554	16	US-10-412-699B-161	Sequence 1691, Ap
45	18	60.0	442	9	US-09-867-550-1691	

ALIGNMENTS

RESULT 1
US-10-425-821-93/c
; Sequence 93, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos'e
; APPLICANT: BEKAL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425, 821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-93

Query Match	100.0%	Score 30:	DB 18:	Length 502:
Best Local Similarity	100.0%	Pred. No. 0.0041:		
Matches	30:	Conservative 0:	Mismatches 0:	Gaps 0:
Qy	1	CTGTCAAGTAACAACCGTAACATCGCTC	30	
Db	499	CTGTCAAGTAACAACCGTAACATCGCTC	470	
RESULT 2	US-10-765-580-9/c			
	; Sequence 9, Application US/10765580			
	; Publication No. US2004016555A1			
	; GENERAL INFORMATION:			
	; APPLICANT: Backer, Marina V.			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 2064.9 seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-5

Perfect score: 30
Sequence: 1 ctgcacagtaacacgcgtacatcgctc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ggsl:*
9: gb_ggsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	164	4	BG384763 304043 MA
2	21.2	70.7	368	8	AZ025072 RPT-23-3
3	21.2	70.7	503	8	AZ018631 RPT-23-3
4	21.2	70.7	529	8	AZ282444 RPT-23-1
5	21.2	70.7	773	8	AZ086094 RPT-23-2
6	20.8	69.3	1055	9	CG882376 ZMBB049
7	20.6	68.7	521	5	BM300571 BM300571
8	20.6	68.7	638	5	BM170815 BM170815
9	20.2	67.3	586	8	AQ46724 RPT-11-12
10	20.2	67.3	649	1	AV690243 AV690243
11	20	66.7	293	4	BI282542 UI-R-DD0-
12	20	66.7	410	1	A1716987 UI-R-Y0-a
13	20	66.7	432	5	BP015197 BP015197
14	20	66.7	479	2	BF524053 UI-R-Y0-a
15	20	66.7	843	9	CNS0477S Tetraodon
16	20	66.7	1020	9	CNS02MMM Tetraodon
17	19.8	66.0	504	8	BZ675685 PUBH667D
18	19.8	66.0	772	8	CC446311 PUBH667D
19	19.6	65.3	466	8	BU086125 SNEST4B03
20	19.6	65.3	702	8	BH056260 RPT-24-3
21	19.6	65.3	1053	9	CG905026 ZMBB051
22	19.4	64.7	1101	9	CNS00DB2 AL067118 Drosophila
23	19.4	64.7	285	2	BE586828 WHE0508 F
24	19.4	64.7	464	2	AMS61714 AMS61714

25	19.4	64.7	467	7	CN813395
26	19.4	64.7	476	7	CN812458
27	19.4	64.7	478	6	CB731532
28	19.4	64.7	485	7	CN811481
29	19.4	64.7	499	7	CR469740
30	19.4	64.7	503	7	CN812532
31	19.4	64.7	503	7	CN812533
32	19.4	64.7	589	2	BS360698
33	19.4	64.7	623	4	BU591342
34	19.4	64.7	623	4	BU591342
35	19.4	64.7	650	8	AO649119
36	19.4	64.7	654	9	CE847863
37	19.4	64.7	660	4	BU610625
38	19.4	64.7	665	4	BU580557
39	19.4	64.7	667	4	BU608742
40	19.4	64.7	679	8	BH955021
41	19.4	64.7	680	4	BU590971
42	19.4	64.7	684	9	CG031879
43	19.4	64.7	715	4	BU587143
44	19.4	64.7	744	4	BU596867
45	19.4	64.7	799	8	CC085595
			820	5	BU326276

ALIGNMENTS

RESULT 1
LOCUS BG384763 164 bp mRNA linear EST 12-MAR-2001
DEFINITION BG384763
ACCESSION BG384763.1 GI:13309235
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 164)
Fahnenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Petrea,G., Sultana,R.,
Quackenbush,J. and Keefe,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
12226715

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -primatch 12 options.
PCR primers: AGGAACAGTATGACCAT
FORWARD: GTTTCACGTACGACG
BACKWARD: GTTTCACGTACGACG
Plate: 92 row: P column: 18
Seq primer: ATTGAGGACATATAG.
Location/Qualifiers
1..164
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="RDH10B"
/clone_lib="MARC 1P1G"
/note="Vector: PCMV SPORF6; Site_1: NotI; Site_2: SalI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 195.093 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-6
Perfect score: 24
Sequence: 1 tgcacacagctgcgtcagtaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	502	18	US-10-425-821-93
2	24	100.0	879	17	US-10-765-580-9
3	24	100.0	945	9	US-09-334-477-1
4	24	100.0	969	9	US-09-334-477-20
5	24	100.0	981	9	US-09-334-477-36
6	24	100.0	1241	9	US-09-334-477-9
7	24	100.0	1507	17	US-10-765-580-11
8	24	100.0	2073	9	US-09-334-477-46
9	24	100.0	2127	9	US-09-334-477-32
10	24	100.0	48908	14	US-10-114-170-137
11	24	100.0	75.8	18	US-10-425-115-147290
12	18.2	75.8	37487	16	US-10-394-948-22

C 13	18.2	75.8	37487	16	US-10-052-482-4	Sequence 4, Appli
C 14	17.6	73.3	154	18	US-10-425-115-16664	Sequence 16664, A
C 15	17.6	73.3	341	16	US-10-424-599-85169	Sequence 85169, A
C 16	17.6	73.3	1217	17	US-10-451-467A-83	Sequence 83, Appli
C 17	17.4	72.5	233	17	US-10-767-701-15871	Sequence 15871, A
C 18	17.4	72.5	611	13	US-10-027-632-189630	Sequence 189630,
C 19	17.4	72.5	611	13	US-10-027-632-189631	Sequence 189631,
C 20	17.4	72.5	611	13	US-10-027-632-189630	Sequence 189630,
C 21	17.4	72.5	611	15	US-10-027-632-189631	Sequence 189631,
C 22	17.2	71.7	567	17	US-10-767-701-26714	Sequence 26714, A
C 23	17.2	71.7	633	13	US-10-027-632-26101	Sequence 26101, A
C 24	17.2	71.7	684	15	US-10-027-632-26101	Sequence 26101, A
C 25	17.2	71.7	684	15	US-10-172-118-2169	Sequence 2169, Ap
C 26	17.2	71.7	684	16	US-10-342-887-2169	Sequence 2169, Ap
C 27	17.2	71.7	1519	16	US-10-425-114-26755	Sequence 26755, A
C 28	17.2	71.7	1571	18	US-10-425-115-41305	Sequence 41305, A
C 29	17.2	71.7	10853	18	US-10-723-860-6115	Sequence 6115, Ap
C 30	17.2	71.7	66884	18	US-10-719-993-7036	Sequence 7036, Ap
C 31	17.2	71.7	15554	13	US-10-087-192-391	Sequence 391, App
C 32	16.8	70.0	588	16	US-10-424-599-20612	Sequence 20612, A
C 33	16.8	70.0	1146	9	US-10-357-930-58838	Sequence 58838, A
C 34	16.8	70.0	1146	9	US-09-810-936-9	Sequence 9, Appli
C 35	16.8	70.0	1146	9	US-09-429-755-9	Sequence 9, Appli
C 36	16.8	70.0	1146	9	US-09-924-400-9	Sequence 9, Appli
C 37	16.8	70.0	1146	15	US-10-212-679-9	Sequence 9, Appli
C 38	16.8	70.0	1146	16	US-10-079-137B-9	Sequence 9, Appli
C 39	16.8	70.0	3646	9	US-09-810-936-227	Sequence 227, App
C 40	16.8	70.0	3646	9	US-09-429-755-227	Sequence 227, App
C 41	16.8	70.0	3646	15	US-09-924-400-227	Sequence 227, App
C 42	16.8	70.0	3646	15	US-10-212-679-227	Sequence 227, App
C 43	16.8	70.0	3646	16	US-10-079-137B-227	Sequence 227, App
C 44	16.8	70.0	9388	9	US-09-810-936-141	Sequence 141, App
C 45	16.8	70.0	9388	9	US-09-429-755-141	Sequence 141, App

ALIGNMENTS

```

US-10-425-821-93/c
Sequence 93, Application US/10425821
Publication No. US20040219530A1
GENERAL INFORMATION:
APPLICANT: BROUSSEAU, Roland
APPLICANT: HAREL, Jose
APPLICANT: BEKAL, Sadia
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCE: 86369-3
CURRENT APPLICATION NUMBER: US/10/425, 821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93
LENGTH: 502
TYPE: DNA
ORGANISM: Escherichia coli
US-10-425-821-93

Query Match      100.0%; Score 24; DB 18; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCACAGACTGCTCAGTAGGT 24
      |||||
DB      468 TGCACAGACTGCTCAGTAGGT 445

RESULT 2
US-10-765-580-9/c
Sequence 9, Application US/10765580
Publication No. US2004016565A1
GENERAL INFORMATION:
APPLICANT: Backer, Marina V.

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 / Search time 37.3454 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23
Sequence: 1 agcagaagccttaccgagc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	954	3	US-08-816-977-5
2	23	100.0	954	4	US-09-334-477-5
3	23	100.0	981	3	US-08-816-977-24
4	23	100.0	981	4	US-09-334-477-24
5	23	100.0	990	4	US-08-816-977-38
6	23	100.0	990	4	US-09-334-477-38
7	23	100.0	1235	4	US-08-816-977-10
8	23	100.0	1235	4	US-09-334-477-10
9	23	100.0	1254	4	US-09-599-032A-3
10	23	100.0	2085	3	US-08-816-977-48
11	23	100.0	2085	4	US-09-334-477-48
12	23	100.0	2136	4	US-08-816-977-34
13	23	100.0	2136	4	US-09-334-477-34
14	23	100.0	61663	3	US-09-453-702B-62
15	17.2	74.8	2430	2	US-08-820-170A-35
16	17.2	74.8	2430	3	US-09-055-699-35
17	17.2	74.8	2430	3	US-09-273-565-35
18	17.2	74.8	2430	3	US-09-565-538-35
19	17.2	74.8	2430	3	US-09-661-468-35
20	17.2	74.8	2430	3	US-09-976-165-35
21	17.2	74.8	2977	2	US-08-820-170A-36
22	17.2	74.8	2977	3	US-09-055-699-36
23	17.2	74.8	2977	3	US-09-273-565-36
24	17.2	74.8	2977	3	US-09-565-538-36
25	17.2	74.8	2977	3	US-09-661-468-36
26	17.2	74.8	2977	4	US-09-976-165-36
27	16.6	72.2	1699	3	US-09-058-260-13

28	16.6	72.2	1753	3	US-09-058-260-21	Sequence 21, Appl
29	16.6	72.2	1756	3	US-09-058-260-31	Sequence 31, Appl
30	16.6	72.2	1766	3	US-09-058-260-23	Sequence 23, Appl
31	16.6	72.2	1896	3	US-09-058-260-3	Sequence 3, Appl
32	16.6	72.2	1925	3	US-09-058-260-17	Sequence 17, Appl
33	16.6	72.2	1952	3	US-09-058-260-5	Sequence 5, Appl
34	16.6	72.2	1957	3	US-09-058-260-19	Sequence 19, Appl
35	16.6	72.2	4090	2	US-08-781-802-5	Sequence 5, Appl
36	16.6	72.2	4090	3	US-08-694-078-5	Sequence 5, Appl
37	16.6	72.2	6263	2	US-08-781-802-3	Sequence 3, Appl
38	16.6	72.2	6263	3	US-08-694-078-3	Sequence 3, Appl
39	16.2	70.4	12752	2	US-08-459-146-1	Sequence 1, Appl
40	16.2	70.4	12752	2	US-08-459-065-1	Sequence 1, Appl
41	15.8	67.7	1830121	4	US-09-557-884-1	Sequence 1, Appl
42	15.8	67.7	1830121	4	US-09-643-990A-1	Sequence 1, Appl
43	15.8	67.7	1830121	4	US-10-339-960-1	Sequence 1, Appl
44	15.6	67.8	885	4	US-09-328-352-3400	Sequence 3400, Ap
45	15.6	67.8	1212	4	US-09-489-039A-4710	Sequence 4710, Ap

ALIGNMENTS

RESULT 1
US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Rugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPND-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 23; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 186.964 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcagaagccttacgcttcagc 23

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	23	100.0	482 18 US-10-425-821-94	Sequence 94, Appl
2	23	100.0	954 9 US-09-334-477-5	Sequence 5, Appl
3	23	100.0	981 9 US-09-334-477-24	Sequence 24, Appl
4	23	100.0	990 9 US-09-334-477-38	Sequence 38, Appl
5	23	100.0	1235 9 US-09-334-477-10	Sequence 10, Appl
6	23	100.0	1612 9 US-09-870-759-27	Sequence 27, Appl
7	23	100.0	1612 10 US-09-751-708A-27	Sequence 27, Appl
8	23	100.0	1612 18 US-10-428-817A-23	Sequence 23, Appl
9	23	100.0	1612 18 US-10-425-821-92	Sequence 92, Appl
10	23	100.0	2085 9 US-09-334-477-48	Sequence 48, Appl
11	23	100.0	2136 9 US-09-334-477-34	Sequence 34, Appl
12	23	100.0	61662 16 US-10-418-837-1	Sequence 1, Appl

13	23	100.0	61663 14 US-10-114-170-62	Sequence 62, Appl
14	18.2	79.1	543 13 US-10-027-632-48009	Sequence 48009, A
15	18.2	79.1	543 13 US-10-027-632-48010	Sequence 48010, A
16	18.2	79.1	543 15 US-10-027-632-48009	Sequence 48009, A
17	18.2	79.1	543 15 US-10-027-632-48010	Sequence 48010, A
18	18.2	79.1	620 13 US-10-027-632-62196	Sequence 62196, A
19	18.2	79.1	620 13 US-10-027-632-62197	Sequence 62197, A
20	18.2	79.1	620 13 US-10-027-632-62198	Sequence 62198, A
21	18.2	79.1	620 13 US-10-027-632-62199	Sequence 62199, A
22	18.2	79.1	620 13 US-10-027-632-62198	Sequence 62198, A
23	18.2	79.1	620 13 US-10-027-632-62199	Sequence 62199, A
24	18.2	79.1	620 13 US-10-027-632-62198	Sequence 62198, A
25	18.2	79.1	620 13 US-10-027-632-62199	Sequence 62199, A
26	18.2	79.1	620 15 US-10-027-632-62196	Sequence 62196, A
27	18.2	79.1	620 15 US-10-027-632-62197	Sequence 62197, A
28	18.2	79.1	620 15 US-10-027-632-62198	Sequence 62198, A
29	18.2	79.1	620 15 US-10-027-632-62199	Sequence 62199, A
30	18.2	79.1	620 15 US-10-027-632-62196	Sequence 62196, A
31	18.2	79.1	620 15 US-10-027-632-62197	Sequence 62197, A
32	18.2	79.1	620 15 US-10-027-632-62198	Sequence 62198, A
33	18.2	79.1	620 15 US-10-027-632-62199	Sequence 62199, A
34	18.2	79.1	1102 15 US-10-027-632-63110	Sequence 63110, A
35	18.2	79.1	1102 15 US-10-027-632-63111	Sequence 63111, A
36	17.2	74.8	300 18 US-10-425-115-109357	Sequence 109357, A
37	17.2	74.8	642 18 US-10-425-115-63775	Sequence 63775, A
38	17.2	74.8	743 13 US-10-027-632-53457	Sequence 53457, A
39	17.2	74.8	743 13 US-10-027-632-53457	Sequence 53457, A
40	17.2	74.8	1197 18 US-10-425-115-5246	Sequence 5246, A
41	17.2	74.8	1421 17 US-10-717-597-60	Sequence 60, Appl
42	17.2	74.8	2430 15 US-10-342-276-35	Sequence 35, Appl
43	17.2	74.8	2977 9 US-09-976-165-35	Sequence 35, Appl
44	17.2	74.8	2977 9 US-09-976-165-35	Sequence 35, Appl
45	17.2	74.8	2977 9 US-09-954-456-735	Sequence 735, Appl

ALIGNMENTS

US-10-425-821-94
; Sequence 94, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos'e
; APPLICANT: BEKAL, Sadia
; TITLE OF INVENTION: ARRAY AND USBS THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-94

Query Match 100.0%; Score 23; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGAAGCCTTACGCTTCAGGC 23
DB 414 AGCAGAAGCCTTACGCTTCAGGC 436

RESULT 2
US-09-334-477-5
; Sequence 5, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 819.794 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagttctgcgtttgtcactgtca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenBank: 1: gb ba: *
2: gb_ptg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	AX106739	Sequence
2	28	100.0	954	AR099864	Sequence
3	28	100.0	954	AR431398	Sequence
4	28	100.0	963	CFSLTITICA	Sequence
5	28	100.0	981	AR099878	Sequence
6	28	100.0	981	AR431412	Sequence
7	28	100.0	990	AR099887	Sequence
8	28	100.0	990	AR431421	Sequence
9	28	100.0	1193	AF298816	Sequence
10	28	100.0	1220	AB048835	Sequence
11	28	100.0	1220	AB048836	Sequence
12	28	100.0	1220	AB048837	Sequence
13	28	100.0	1224	AB048239	Sequence
14	28	100.0	1235	AR099867	Sequence
15	28	100.0	1235	AR431401	Sequence
16	28	100.0	1236	ECED42SLT	Sequence
17	28	100.0	1236	ECED43SLT	Sequence
18	28	100.0	1236	ECED53SLT	Sequence
19	28	100.0	1236	ECED68SLT	Sequence

20	28	100.0	1237	1	AB048240	Escherich
21	28	100.0	1241	1	AB048233	Escherich
22	28	100.0	1241	1	ECOT272135	Escherich
23	28	100.0	1241	6	E03959	The VT2 gen
24	28	100.0	1241	6	E03962	The VT2 gen
25	28	100.0	1241	7	AY633453	Bacteriop
26	28	100.0	1241	7	AY633454	Bacteriop
27	28	100.0	1241	7	AY633455	Bacteriop
28	28	100.0	1241	7	AY633456	Bacteriop
29	28	100.0	1241	7	AY633457	Bacteriop
30	28	100.0	1241	7	AY633458	Bacteriop
31	28	100.0	1241	7	AY633459	Bacteriop
32	28	100.0	1241	7	AY633460	Bacteriop
33	28	100.0	1241	7	AY633461	Bacteriop
34	28	100.0	1241	7	AY633462	Bacteriop
35	28	100.0	1241	7	AY633463	Bacteriop
36	28	100.0	1241	7	AY633464	Bacteriop
37	28	100.0	1241	7	AY633465	Bacteriop
38	28	100.0	1241	7	AY633466	Bacteriop
39	28	100.0	1241	7	AY633467	Bacteriop
40	28	100.0	1241	7	AY633468	Bacteriop
41	28	100.0	1241	7	AY633469	Bacteriop
42	28	100.0	1241	7	AY633470	Bacteriop
43	28	100.0	1241	7	AY633471	Bacteriop
44	28	100.0	1241	7	AY633472	Bacteriop
45	28	100.0	1241	7	AY633473	Bacteriop

ALIGNMENTS

RESULT 1	AX106739	Sequence 7 from Patent WO0123607.	28 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106739					
DEFINITION	AX106739					
ACCESSION	AX106739.1	GI:13922400				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Db						
Qy						
RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
Unclassified.						

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 227.608 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagcttcgcttgcctcactgca 28

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	482	18	US-10-425-821-94
2	28	100.0	954	9	US-09-334-477-5
3	28	100.0	981	9	US-09-334-477-24
4	28	100.0	990	9	US-09-334-477-38
5	28	100.0	1235	9	US-09-334-477-10
6	28	100.0	1612	9	US-09-870-759-27
7	28	100.0	1612	10	US-09-751-708A-27
8	28	100.0	1612	18	US-10-428-817A-23
9	28	100.0	1612	18	US-10-425-821-92
10	28	100.0	2085	9	US-09-334-477-48
11	28	100.0	2136	9	US-09-334-477-34
12	28	100.0	61662	16	US-10-418-837-1

13	28	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl
14	24	85.7	39	14	US-10-085-056-35	Sequence 35, Appl
15	20.6	73.6	1030	9	US-09-945-376-3	Sequence 3, Appl
16	20	71.4	1323	15	US-10-369-493-32410	Sequence 3410, A
17	19.2	68.6	47443	11	US-09-997-722-94	Sequence 94, Appl
18	19	67.9	474	13	US-10-027-632-129849	Sequence 129849, A
19	19	67.9	474	15	US-10-027-632-129849	Sequence 129849, A
20	19	67.9	13440	15	US-10-213-948-12	Sequence 12, Appl
21	18.6	66.4	444	18	US-10-357-930-13108	Sequence 13108, A
22	18.4	65.7	113	15	US-10-029-386-26028	Sequence 26028, A
23	18.4	65.7	505	15	US-10-425-115-11289	Sequence 11289, A
24	18.4	65.7	568	15	US-10-029-386-12328	Sequence 12328, A
25	18.4	65.7	640	13	US-10-027-632-137774	Sequence 137774, A
26	18.4	65.7	640	15	US-10-027-632-137774	Sequence 137774, A
27	18.4	65.7	774	13	US-10-027-632-137773	Sequence 137773, A
28	18.4	65.7	774	15	US-10-027-632-137773	Sequence 137773, A
29	18.4	65.7	1161	16	US-10-425-114-29267	Sequence 29267, A
30	18.4	65.7	1161	18	US-10-425-114-133253	Sequence 143253, A
31	18.2	65.0	2385	16	US-10-282-122A-32403	Sequence 32403, A
32	18.2	65.0	3106	13	US-10-027-632-113748	Sequence 113748, A
33	18.2	65.0	3106	15	US-10-027-632-113748	Sequence 113748, A
34	18	64.3	5885	16	US-10-062-674-11770	Sequence 11770, Ap
35	18	64.3	83719	17	US-10-388-838-45	Sequence 45, Appl
36	18	64.3	197997	9	US-09-822-246-3	Sequence 3, Appl
37	18	64.3	197997	18	US-10-469-028-3	Sequence 3, Appl
38	18	64.3	684187	17	US-10-367-094-71	Sequence 71, Appl
39	17.8	63.6	448	10	US-09-918-995-35148	Sequence 35148, A
40	17.8	63.6	3833	15	US-10-104-047-339	Sequence 339, App
41	17.8	63.6	4816	18	US-10-357-930-23466	Sequence 23466, A
42	17.8	63.6	4816	18	US-10-357-930-29353	Sequence 29353, A
43	17.6	62.9	405	9	US-09-918-995-3446	Sequence 3446, Ap
44	17.6	62.9	407	9	US-09-764-877-667	Sequence 667, App
45	17.6	62.9	407	16	US-10-242-515-667	Sequence 667, App

ALIGNMENTS

RESULT 1
US-10-425-821-94
; Sequence 94, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos'e
; APPLICANT: BEKAL, Sadia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-10-425-821-94

Query Match 100.0%; Score 28; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.012; 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGCAGTTCGCTTGTGTCACATGCA 28
DB 365 AGAGCAGTTCGCTTGTGTCACATGCA 412

RESULT 2
US-09-334-477-5
; Sequence 5, Application US/09334477
; Patent No. US20020012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 614.845 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21
Sequence: 1 CGATCTCCGAGACATG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenDbml:*

- 1: gb_da:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_stb:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	21	100.0	21	6	AX106736
2	21	100.0	954	6	AR099864 Sequence
3	21	100.0	954	6	AR431398 Sequence
4	21	100.0	963	1	CFSLTICA
5	21	100.0	981	6	AR099878 Sequence
6	21	100.0	981	6	AR431412 Sequence
7	21	100.0	990	6	AR099887 Sequence
8	21	100.0	990	6	AR431421 Sequence
9	21	100.0	1220	1	AB048835
10	21	100.0	1220	1	AB048836
11	21	100.0	1220	1	AB048837
12	21	100.0	1224	1	AB048239
13	21	100.0	1235	6	AR099867 Sequence
14	21	100.0	1235	6	AR431401
15	21	100.0	1236	1	ECED42ST
16	21	100.0	1236	1	ECED43SLT
17	21	100.0	1236	1	ECED53SLT
18	21	100.0	1236	1	ECED68SLT
19	21	100.0	1237	1	AB048240

C	20	21	100.0	1241	1	AB048233	AB048233 Escherich
C	21	21	100.0	1241	1	EC0272135	AJ272135 Escherich
C	22	21	100.0	1241	6	E03959	E03959 The VT2 gen
C	23	21	100.0	1241	6	E03962	E03962 The VT2 gen
C	24	21	100.0	1241	7	AY633453	AY633453 Bacteriop
C	25	21	100.0	1241	7	AY633454	AY633454 Bacteriop
C	26	21	100.0	1241	7	AY633455	AY633455 Bacteriop
C	27	21	100.0	1241	7	AY633456	AY633456 Bacteriop
C	28	21	100.0	1241	7	AY633457	AY633457 Bacteriop
C	29	21	100.0	1241	7	AY633458	AY633458 Bacteriop
C	30	21	100.0	1241	7	AY633459	AY633459 Bacteriop
C	31	21	100.0	1241	7	AY633460	AY633460 Bacteriop
C	32	21	100.0	1241	7	AY633461	AY633461 Bacteriop
C	33	21	100.0	1241	7	AY633462	AY633462 Bacteriop
C	34	21	100.0	1241	7	AY633463	AY633463 Bacteriop
C	35	21	100.0	1241	7	AY633464	AY633464 Bacteriop
C	36	21	100.0	1241	7	AY633465	AY633465 Bacteriop
C	37	21	100.0	1241	7	AY633466	AY633466 Bacteriop
C	38	21	100.0	1241	7	AY633467	AY633467 Bacteriop
C	39	21	100.0	1241	7	AY633468	AY633468 Bacteriop
C	40	21	100.0	1241	7	AY633469	AY633469 Bacteriop
C	41	21	100.0	1241	7	AY633470	AY633470 Bacteriop
C	42	21	100.0	1241	7	AY633471	AY633471 Bacteriop
C	43	21	100.0	1241	7	AY633472	AY633472 Bacteriop
C	44	21	100.0	1241	7	AY633473	AY633473 Bacteriop
C	45	21	100.0	1242	1	AB048227	AB048227 Escherich

ALIGNMENTS

RESULT 1	AX106736	21 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106736	Sequence 4 from Patent WO0123607.			
DEFINITION	AX106736				
ACCESSION	AX106736				
VERSION	AX106736.1	GI:13922397			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 21;	DB 6;	Length 21;	
Best Local Similarity	100.0%;	Pred. No. 0.66;			
Matches	21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Cy	1	CGATACTCCGAGACATG	21		
Db	1	CGATACTCCGAGACATG	21		
RESULT 2	AR099864/c	954 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099864	Sequence 5 from patent US 6080400.			
DEFINITION	AR099864				
ACCESSION	AR099864				
VERSION	AR099864.1	GI:12810312			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 585.567 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-3

Perfect score: 20

Sequence: 1 ttccggaatgcaatcagtc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_da: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6 AX106735	AX106735 Sequence
2	20	100.0	34	6 AX698158	AX698158 Sequence
3	20	100.0	151	7 BF6251234	BF6251234 Bacterioph
4	20	100.0	152	7 BF5251233	BF5251233 Bacterioph
5	20	100.0	153	7 BF3251232	BF3251232 Bacterioph
6	20	100.0	157	7 BF1251231	BF1251231 Bacterioph
7	20	100.0	294	1 ECU41241	ECU41241 Escherichia
8	20	100.0	296	1 ECU41240	ECU41240 Escherichia
9	20	100.0	298	1 ECU41236	ECU41236 Escherichia
10	20	100.0	298	1 ECU41238	ECU41238 Escherichia
11	20	100.0	299	1 ECU41235	ECU41235 Escherichia
12	20	100.0	307	1 ECU41242	ECU41242 Escherichia
13	20	100.0	310	1 ECU41239	ECU41239 Escherichia
14	20	100.0	312	1 ECU41237	ECU41237 Escherichia
15	20	100.0	320	1 ECU41243	ECU41243 Escherichia
16	20	100.0	329	1 ECU41244	ECU41244 Escherichia
17	20	100.0	439	1 AB119450	AB119450 Escherich
18	20	100.0	439	1 AB119451	AB119451 Escherich
19	20	100.0	439	1 AB119452	AB119452 Escherich

20	20	100.0	439	1	AB119453	AB119453 Escherich
21	20	100.0	439	1	AB119454	AB119454 Escherich
22	20	100.0	439	1	AB119455	AB119455 Escherich
23	20	100.0	439	1	AB119456	AB119456 Escherich
24	20	100.0	439	1	AB119457	AB119457 Escherich
25	20	100.0	439	1	AB119458	AB119458 Escherich
26	20	100.0	439	1	AB119459	AB119459 Escherich
27	20	100.0	439	1	AB119460	AB119460 Escherich
28	20	100.0	487	1	AF378101	AF378101 Escherich
29	20	100.0	515	1	AF532128	AF532128 Escherich
30	20	100.0	540	6	E66869	E66869 Method for
31	20	100.0	540	6	E66923	E66923 Method for
32	20	100.0	540	6	AR210788	AR210788 Sequence
33	20	100.0	954	6	AR099864	AR099864 Sequence
34	20	100.0	954	6	AR431398	AR431398 Sequence
35	20	100.0	963	1	CBSLITICA	X67514 C firendi
36	20	100.0	981	6	AR099878	AR099878 Sequence
37	20	100.0	981	6	AR431412	AR431412 Sequence
38	20	100.0	990	6	AR099887	AR099887 Sequence
39	20	100.0	990	6	AR431421	AR431421 Sequence
40	20	100.0	1193	1	AF298816	AF298816 Escherich
41	20	100.0	1220	1	AB048835	AB048835 Escherich
42	20	100.0	1220	1	AB048836	AB048836 Escherich
43	20	100.0	1220	1	AB048837	AB048837 Escherich
44	20	100.0	1224	1	AB048239	AB048239 Escherich
45	20	100.0	1235	6	AR099867	AR099867 Sequence

ALIGNMENTS

RESULT 1
AX106735
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX106735
Sequence 3 from Patent WO0123607.
AX106735
AX106735.1 GI:13922396
Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

1
Gruner, F. and Bellin, T.
Multiplex PCR for detecting ehc infections
Patent: WO 013607-A 3 05-APR-2001;
Roche Diagnostics GmbH (DE)
Location/Qualifiers
1..20
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGAATGCAATCAGTC 20
DB 1 TTCCGGAATGCAATCAGTC 20

RESULT 2
AX698158/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX698158
Sequence 7 from Patent WO03010332.
AX698158
AX698158.1 GI:29499167
synthetic construct
synthetic construct
artificial sequences.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-2

Perfect score: 24

Sequence: 1 ccgacacatgaaggaactcat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ha: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sgs: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6	AX106734 Sequence
2	24	100.0	945	6	AR099862 Sequence
3	24	100.0	945	6	AR431396 Sequence
4	24	100.0	948	1	AB071619 Sequence
5	24	100.0	969	6	AR099876 Sequence
6	24	100.0	969	6	AR431410 Sequence
7	24	100.0	981	6	AR099886 Sequence
8	24	100.0	981	6	AR431420 Sequence
9	24	100.0	1238	1	AB015056 Sequence
10	24	100.0	1238	1	AB030485 Sequence
11	24	100.0	1238	1	AB048232 Sequence
12	24	100.0	1241	6	AR099866 Sequence
13	24	100.0	1241	6	AR431400 Sequence
14	24	100.0	1297	1	AB035142 Sequence
15	24	100.0	1320	1	SDFOXAB Sequence
16	24	100.0	1362	6	SS0132761 Sequence
17	24	100.0	1369	6	E27911 Method for
18	24	100.0	1433	1	ECSLTABA
19	24	100.0	1433	1	ECSLTABA

c 20	24	100.0	1499	7	J93SLTI	M19473 Bacterioph
c 21	24	100.0	1500	1	SHPSHT	M19437 S.dysenteri
c 22	24	100.0	1591	7	H19BSLT	M16625 Bacterioph
c 23	24	100.0	1601	1	AF461166	AF461166 Escherich
c 24	24	100.0	1601	1	AF461168	AF461168 Escherich
c 25	24	100.0	1601	1	AF461169	AF461169 Escherich
c 26	24	100.0	1710	7	H19BSLT	M19358 Bacterioph
c 27	24	100.0	1905	7	H30SLT	M23980 Bacterioph
c 28	24	100.0	1956	1	AR461172	AR461172 Escherich
c 29	24	100.0	2073	6	AR099894	AR099894 Sequence
c 30	24	100.0	2073	6	AR431428	AR431428 Sequence
c 31	24	100.0	2127	6	AR099884	AR099884 Sequence
c 32	24	100.0	2127	6	AR431418	AR431418 Sequence
c 33	24	100.0	2540	1	AB083043	AB083043 Escherich
c 34	24	100.0	3294	1	SHPSHT	M23352 S.dysenteri
c 35	24	100.0	5467	1	ECO251325	AJ251325 Escherich
c 36	24	100.0	5567	1	ECOSLTI	L04539 Escherich
c 37	24	100.0	6014	1	SDY271153	AJ771153 Shigella
c 38	24	100.0	6921	7	ECO413275	AJ713275 Bacterioph
c 39	24	100.0	8053	7	SSO279086	AJ779086 Shigella
c 40	24	100.0	10127	1	AE005442	AE005442 Escherich
c 41	24	100.0	18362	7	AF034975	AF034975 Bacterioph
c 42	24	100.0	31831	1	ECO304858	AJ034858 Escherich
c 43	24	100.0	32094	1	AF153317	AF153317 Shigella
c 44	24	100.0	47879	6	BD184771	BD184771 Nucleic a
c 45	24	100.0	48908	6	AR204241	AR204241 Sequence

ALIGNMENTS

RESULT 1	AX106734	Sequence 2 from Patent WO01233607.	24 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106734					
DEFINITION	AX106734					
ACCESSION	AX106734.1	GI:13922395				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
Source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Conservative						
Mismatches						
Indels						
Gaps						
DB						
CCGACACATGGAAGAACTCAT						
RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
Unknown.						
Unclassified.						

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 184.701 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24

Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_23Sep04:*

1: Geneseq19808:*\n2: Geneseq19908:*\n3: Geneseq20008:*\n4: Geneseq20018:*\n5: Geneseq20018:*\n6: Geneseq20028:*\n7: Geneseq20028:*\n8: Geneseq20038:*\n9: Geneseq20038:*\n10: Geneseq20038:*\n11: Geneseq20038:*\n12: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	24	5	AA61483	Aa61483 EHEC huma
2	100.0	43	2	AAT97605	Aat97605 Shigella
3	100.0	287	12	ADN02037	Adn02037 Enterohae
4	100.0	870	10	AD14887	Ad14887 DNA encod
5	100.0	945	2	AAT42649	Aat42649 Verotoxig
6	100.0	945	2	AA51194	AA51194 E. coli v
7	100.0	945	6	ABK11775	Abk11775 E. coli v
8	100.0	948	4	AAH01085	Aah01085 Escherich
9	100.0	969	2	AAT42663	Aat42663 Histidine
10	100.0	969	3	AA51208	AA51208 Recombina
11	100.0	969	6	ABK11789	Abk11789 CDNA enco
12	100.0	980	2	AAT42673	Aat42673 FLAG tag/
13	100.0	981	6	AA51218	AA51218 FLAG tag-
14	100.0	1192	2	AAV11402	Aav11402 Shiga tox
15	100.0	1192	2	AAV11403	Aav11403 Shiga tox
16	100.0	1227	11	AD125576	Ad125576 S. dysent
17	100.0	1227	11	AD125577	Ad125577 S. sonnei
18	100.0	1227	11	AD125578	Ad125578 Bacteriop
19	100.0	1227	11	AAQ12711	Aaq12711 Shiga-11k
20	100.0	1230	2	AAQ12711	Aaq12711 Shiga-11k
21	100.0	1230	2	AAT91637	Aat91637 Phage H19

C 22	24	100.0	1230	2	AA230662	Aa230662 E.coli ba
C 23	24	100.0	1230	3	AA290018	Aa290018 E. coli b
C 24	24	100.0	1235	2	AAV11404	Aav11404 Shiga tox
C 25	24	100.0	1241	2	AA42653	Aat42653 Sequence
C 26	24	100.0	1241	2	AA51198	AA51198 DNA direc
C 27	24	100.0	1241	6	ABK11779	Abk11779 Polycistr
C 28	24	100.0	1369	2	AA227687	Aa227687 Verotoxin
C 29	24	100.0	1389	2	AAV11400	Aav11400 Shiga tox
C 30	24	100.0	2073	3	AA51226	AA51226 MBP-VT-1
C 31	24	100.0	2073	6	ABK11957	Abk11957 CDNA enco
C 32	24	100.0	2126	2	AAT42671	Aat42671 Maltose b
C 33	24	100.0	2127	3	AA51216	AA51216 MBP-VT-1
C 34	24	100.0	2127	6	ABK11797	Abk11797 CDNA enco
C 35	24	100.0	47879	9	ADC00509	Adc00509 Enterohae
C 36	24	100.0	48908	9	ACD19124	Acid19124 E. coli 0
C 37	19.2	80.0	1188	12	ADU75891	Adu75891 Marker ge
C 38	18.2	75.8	37487	9	ADA02498	Ada02498 Human MYC
C 39	18.2	75.8	37487	10	ADB72236	Adb72236 Human MYC
C 40	18.2	75.8	37487	10	ADE82938	Ad82938 Human MYC
C 41	18.2	75.8	37487	10	ADE95746	Ad95746 Human MYC
C 42	17.6	73.3	1217	6	ABQ76329	Abq76329 S. cerevi
C 43	17.6	73.3	1687	4	AB118110	Ab118110 Drosophi1
C 44	17.6	73.3	1687	4	AB112468	Ab112468 Drosophi1
C 45	17.6	73.3	1687	4	AB118210	Ab118210 Drosophi1

ALIGNMENTS

RESULT 1
ID AAF61483 standard; DNA; 24 BP.
XX AAF61483;
AC AAF61483;
XX
DT 18-JUN-2001 (first entry)
XX
DE EHEC human pathogen strA1 probe SEQ ID 6.
XX
KW EHEC infection; multiplex amplification; detection; human; pig;
XX enterohemorrhagic Escherichia coli infection; pathogen; probe; ss.
XX
OS Escherichia coli.
XX
FN DE19946296-A1.
XX
PD 29-MAR-2001.
XX
PE 28-SEP-1999; 99DE-01046296.
XX
PR 28-SEP-1999; 99DE-01046296.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Gunzer F, Bellin T;
XX WPI; 2001-246145/26.
XX
PT Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
XX in multiplex amplification detection of enterohemorrhagic strains.
XX
PS Claim 11; Page 10; 14pp; German.
XX
CC This invention describes a novel primer (P1) which can be used in a
XX multiplex amplification reaction for detecting clinically important EHEC
XX (enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous
XX detection of human and pig pathogens in a single measurement
XX
SO Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title:	US-10-089-487-1
Perfect score:	24
Sequence:	1 agtcgtacggygatgcagataat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      4526729 segs, 23644849745 residues
Total number of hits satisfying chosen parameters:  9053456
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

```
Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_yy.*
13: gb_un.*
14: gb_vl.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	6	AX106733	AX106733 Sequence
2	24	100.0	39	6	AX524899	AX524899 Sequence
3	24	100.0	39	6	BD174563	BD174563 Oligonuct
4	24	100.0	945	6	AR0998862	AR0998862 Sequence
5	24	100.0	945	6	AR431396	AR431396 Sequence
6	24	100.0	948	1	AB071619	AB071619 Escherich
7	24	100.0	948	1	AB071621	AB071621 Escherich
8	24	100.0	948	1	AB071623	AB071623 Escherich
9	24	100.0	948	6	AX110343	AX110343 Sequence
10	24	100.0	969	6	AR0998875	AR0998875 Sequence
11	24	100.0	969	6	AR431410	AR431410 Sequence
12	24	100.0	981	6	AR099886	AR099886 Sequence
13	24	100.0	981	6	AR431420	AR431420 Sequence
14	24	100.0	1227	1	AB083044	AB083044 Escherich
15	24	100.0	1238	1	AB015056	AB015056 Escherich
16	24	100.0	1238	1	AB030485	AB030485 Escherich
17	24	100.0	1238	1	AB048232	AB048232 Escherich
18	24	100.0	1238	1	AB048235	AB048235 Escherich
19	24	100.0	1239	1	AB048231	AB048231 Escherich

20	24	100.0	1239	1	AB0488237	AB0488237 Escherich
21	24	100.0	1400	1	AB0488234	AB0488234 Escherich
22	24	100.0	1241	6	AR099866	AR099866 Sequence
23	24	100.0	1271	6	AR431400	AR431400 Sequence
24	24	100.0	1241	1	AY170851	AY170851 Escherich
25	24	100.0	1297	1	AB035142	AB035142 Escherich
26	24	100.0	1320	1	SPT0XB	X07903 Shigella dys
27	24	100.0	1338	1	AY135685	AY135685 Escherich
28	24	100.0	1362	1	SS013761	AJ132761 Shigella
29	24	100.0	1369	6	E27911	E27911 Method for
30	24	100.0	1414	7	BE62413986	AJ132966 Bacteriop
31	24	100.0	1432	1	EC0312232	AJ112222 Escherich
32	24	100.0	1432	1	EC0314838	AJ114838 Escherich
33	24	100.0	1432	1	EC0314839	AJ114839 Escherich
34	24	100.0	1433	1	BESLITAB	Z36899 E.coli (ser
35	24	100.0	1433	1	BESLITAB	Z36900 E.coli (ser
36	24	100.0	1434	1	BESLITAB	Z36901 E.coli (ser
37	24	100.0	1499	7	J93SLTI	M19473 Bacterioph
38	24	100.0	1500	1	SHSMT	M14437 S.dysenter
39	24	100.0	1591	7	H19BSLT	M16625 Bacterioph
40	24	100.0	1601	1	AF461166	AF461166 Escherich
41	24	100.0	1601	1	AF461168	AF461168 Escherich
42	24	100.0	1601	1	AF461169	AF461169 Escherich
43	24	100.0	1650	1	AB050958	AB050958 Escherich
44	24	100.0	1650	1	AB050959	AB050959 Escherich
45	24	100.0	1710	7	H19BSLITA	M17358 Bacterioph

ALIGNMENTS

LOCUS	AX106733	24 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 1 from Patent WO0123607.				
ACCESSION	AX106733				
VERSION	AX106733.1	GI:13922394			
KEYWORDS					
SOURCE					
ORGANISM	Escherichia coli				
	Escherichia coli				
	Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
	Enterobacteriaceae; Escherichia.				
REFERENCE	1				
AUTHORS	Gunzer, F. and Bellin, T.				
TITLE	Multiplex pcr for detecting ehec infections				
JOURNAL	Patent: WO 0123607-A 1 05-APR-2001;				
	Roche Diagnostics GmbH (DE)				
FEATURES					
source	location/Qualifiers				
	1..24				
	/organism="Escherichia coli"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:562"				
ORIGIN					
	Query Match	100.0%;	Score 24;	DB 6;	Length 24;
	Best Local Similarity	100.0%;	Fred. No. 0.038;		
	Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 AGTCGTACGGGATGCAGATTAAT 24				
	1 AGTCGTACGGGATGCAGATTAAT 24				
DB					
RESULT 2	AX524899/c				
LOCUS	AX524899	39 bp	DNA	linear	PAT 21-NOV-2002
DEFINITION	Sequence 28 from Patent EP1236806.				
ACCESSION	AX524899				
VERSION	AX524899.1	GI:25169986			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
	synthetic construct				
	artificial sequences.				

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 878.351 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-5
Perfect score: 30
Sequence: 1 ctgtcacagtaacacccgtacatcgctc 30

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 4526729 seqs, 2364489745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_gy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	6	AX106737 Sequence
2	30	100.0	945	6	AR099862 Sequence
3	30	100.0	945	6	AR431396 Sequence
4	30	100.0	948	1	AB071623 Sequence
5	30	100.0	948	6	AX110343 Sequence
6	30	100.0	969	6	AR099876 Sequence
7	30	100.0	969	6	AR431410 Sequence
8	30	100.0	981	6	AR099886 Sequence
9	30	100.0	981	6	AR431420 Sequence
10	30	100.0	1227	1	AB083044 Escherich
11	30	100.0	1238	1	AB015056 Escherich
12	30	100.0	1238	1	AB030485 Escherich
13	30	100.0	1238	1	AB048232 Escherich
14	30	100.0	1238	1	AB048235 Escherich
15	30	100.0	1239	1	AB048231 Escherich
16	30	100.0	1239	1	AB048237 Escherich
17	30	100.0	1240	1	AB048234 Escherich
18	30	100.0	1241	6	AR099866 Sequence
19	30	100.0	1241	6	AR431400 Sequence

c 20	30	100.0	1297	1	AB035142	AB035142 Escherich
c 21	30	100.0	1320	1	SDTOXAB	X07903 Shigella dy
c 22	30	100.0	1338	1	AY135685	AY135685 Escherich
c 23	30	100.0	1362	1	SS0132761	AJ132761 Shigella
c 24	30	100.0	1369	6	E27911	E27911 Method for
c 25	30	100.0	1414	7	B62413986	AJ113986 Bacteriop
c 26	30	100.0	1432	1	ECO312232	AJ12222 Escherich
c 27	30	100.0	1432	1	ECO314838	AJ14838 Escherich
c 28	30	100.0	1432	1	ECO314839	AJ14839 Escherich
c 29	30	100.0	1433	1	EC0314839	Z36899 E.coli (ser
c 30	30	100.0	1433	1	EC0314839	Z36900 E.coli (ser
c 31	30	100.0	1434	1	EC0314839	Z36901 E.coli (ser
c 32	30	100.0	1499	7	J33SLT1	M14973 Bacterioph
c 33	30	100.0	1500	1	SHRSMT	M1437 S.dysenteri
c 34	30	100.0	1591	7	H19BSLT	M1625 Bacterioph
c 35	30	100.0	1601	1	AF461166	AF461166 Escherich
c 36	30	100.0	1601	1	AF461169	AF461169 Escherich
c 37	30	100.0	1710	7	H19BSLT	M17358 Bacterioph
c 38	30	100.0	1905	7	H30SLT	M23980 Bacterioph
c 39	30	100.0	1956	1	AF461172	AF461172 Escherich
c 40	30	100.0	2073	6	AR099894	AR099894 Sequence
c 41	30	100.0	2073	6	AR431428	AR431428 Sequence
c 42	30	100.0	2127	6	AR099884	AR099884 Sequence
c 43	30	100.0	2127	6	AR431418	AR431418 Sequence
c 44	30	100.0	2540	1	AB083043	AB083043 Escherich
c 45	30	100.0				

ALIGNMENTS

RESULT 1
AX106737
LOCUS AX106737 Sequence 5 from Patent WO0123607.
DEFINITION AX106737
ACCESSION AX106737.1 GI:13922398
VERSION
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE
1 Gunzer, F. and Bellin, T.
TITLE Multiplex pcr for detecting ehc infections
JOURNAL Patent: WO 0123607-A 5 05-APR-2001;
Roche Diagnostics GmbH (DE)
FEATURES
SOURCE location/Qualifiers
1..30
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"

ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.012; 0; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;
Oy 1 CTGTACAGTAACACCGTACATCGCTC 30
Db 1 CTGTACAGTAACACCGTACATCGCTC 30
RESULT 2
LOCUS AR099862/c 945 bp. DNA linear PAT 14-FEB-2001
DEFINITION AR099862 Sequence 1 from patent US 6080400.
ACCESSION AR099862
VERSION AR099862.1 GI:12810310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 702.68 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24
Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Genbank1:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	24	100.0	24	AX106738 Sequence
2	24	100.0	43	AR019038 Sequence
3	24	100.0	945	AR099862 Sequence
4	24	100.0	945	AR431396 Sequence
5	24	100.0	948	AB071619 Escherich
6	24	100.0	948	AB071621 Escherich
7	24	100.0	948	AB071623 Escherich
8	24	100.0	948	AX110343 Sequence
9	24	100.0	969	AR099876 Sequence
10	24	100.0	969	AR431410 Sequence
11	24	100.0	981	AR099886 Sequence
12	24	100.0	981	AR431420 Sequence
13	24	100.0	1227	AB083044 Escherich
14	24	100.0	1238	AB015056 Escherich
15	24	100.0	1238	AB030485 Escherich
16	24	100.0	1238	AB048232 Escherich
17	24	100.0	1238	AB048235 Escherich
18	24	100.0	1239	AB048231 Escherich
19	24	100.0	1239	AB048237 Escherich

C 20	24	100.0	1240	1	AB048234	AB048234 Escherich
C 21	24	100.0	1241	6	AR431400	AR099866 Sequence
C 22	24	100.0	1241	6	AR431400	AR431400 Sequence
C 23	24	100.0	1297	1	AB035142	AB035142 Escherich
C 24	24	100.0	1320	1	SDTOXAB	X07903 Shigella dy
C 25	24	100.0	1338	1	AV135685	AV135685 Escherich
C 26	24	100.0	1362	1	SS0132761	AJ132761 Shigella
C 27	24	100.0	1369	6	E27911	E27911 Method for
C 28	24	100.0	1414	7	B62413986	AJ113386 Bacteriop
C 29	24	100.0	1432	1	EC0312232	AJ112232 Escherich
C 30	24	100.0	1432	1	EC0314838	AJ14838 Escherich
C 31	24	100.0	1432	1	EC0314839	AJ14839 Escherich
C 32	24	100.0	1433	1	EC0314839	AJ14839 Escherich
C 33	24	100.0	1433	1	EC0314839	AJ14839 Escherich
C 34	24	100.0	1434	1	EC0314839	AJ14839 Escherich
C 35	24	100.0	1499	7	J93SLTI	Z3690 E.coli (ser
C 36	24	100.0	1500	1	SHFSHT	Z3690 E.coli (ser
C 37	24	100.0	1591	7	H19BSLT	M19437 S.dysenter
C 38	24	100.0	1601	1	AF461166	M16625 Bacterioph
C 39	24	100.0	1601	1	AF461166	AF461166 Escherich
C 40	24	100.0	1601	1	AF461169	AF461169 Escherich
C 41	24	100.0	1710	7	H19BSLT	M19437 S.dysenter
C 42	24	100.0	1905	7	H30SLT	M16625 Bacterioph
C 43	24	100.0	1956	1	AF461172	AF461172 Escherich
C 44	24	100.0	2073	6	AR099894	AR099894 Sequence
C 45	24	100.0	2073	6	AR431428	AR431428 Sequence

ALIGNMENTS

RESULT 1	AX106738	24 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX106738	Sequence 6 from Patent WO0123607.			
DEFINITION	AX106738	AX106738.1 GI:13922399			
ACCESSION	AX106738				
VERSION	AX106738.1	GI:13922399			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TGCACAGACTGCCTCAGTGAGGT 24
Db 1 TGCACAGACTGCCTCAGTGAGGT 24

RESULT 2
AR019038/c
LOCUS AR019038 43 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 18 from patent US 5783196.
ACCESSION AR019038
VERSION AR019038.1 GI:3974152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 38.9691 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24
Sequence: 1 tgcacagactgcgtcagtgaggt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	100.0	43	US-08-629-600-18	Sequence 18, Appl
C 2	24	100.0	945	US-08-816-977-1	Sequence 1, Appl
C 3	24	100.0	945	US-09-334-477-1	Sequence 1, Appl
C 4	24	100.0	969	US-08-816-977-20	Sequence 20, Appl
C 5	24	100.0	969	US-09-334-477-20	Sequence 36, Appl
C 6	24	100.0	981	US-08-816-977-36	Sequence 36, Appl
C 7	24	100.0	981	US-09-334-477-36	Sequence 9, Appl
C 8	24	100.0	1241	US-08-816-977-9	Sequence 9, Appl
C 9	24	100.0	1241	US-09-334-477-9	Sequence 46, Appl
C 10	24	100.0	2073	US-08-816-977-46	Sequence 32, Appl
C 11	24	100.0	2073	US-09-334-477-46	Sequence 32, Appl
C 12	24	100.0	2127	US-08-816-977-32	Sequence 137, App
C 13	24	100.0	2127	US-09-453-7028-137	Sequence 499, App
C 14	24	100.0	48908	US-09-598-326-227	Sequence 227, App
C 15	17.2	71.7	859	US-09-976-594-499	Sequence 9, Appl
C 16	16.8	70.0	1146	US-08-991-789A-9	Sequence 9, Appl
C 17	16.8	70.0	1146	US-09-662-451-9	Sequence 9, Appl
C 18	16.8	70.0	1146	US-09-598-326-9	Sequence 9, Appl
C 19	16.8	70.0	1146	US-09-289-198-9	Sequence 9, Appl
C 20	16.8	70.0	1146	US-09-429-755-9	Sequence 9, Appl
C 21	16.8	70.0	3646	US-08-991-789A-227	Sequence 227, App
C 22	16.8	70.0	3646	US-09-062-451-227	Sequence 227, App
C 23	16.8	70.0	3646	US-09-598-326-227	Sequence 227, App
C 24	16.8	70.0	3646	US-09-289-198-227	Sequence 227, App
C 25	16.8	70.0	3646	US-09-429-755-227	Sequence 227, App
C 26	16.8	70.0	9388	US-08-991-789A-141	Sequence 141, App
C 27	16.8	70.0	9388	US-09-062-451-141	Sequence 141, App

C 28	16.8	70.0	9388	US-09-598-326-141	Sequence 141, App
C 29	16.8	70.0	9388	US-09-289-198-141	Sequence 141, App
C 30	16.8	70.0	9388	US-09-429-755-141	Sequence 141, App
C 31	16.8	70.0	75395	US-09-984-890-3	Sequence 3, Appl
C 32	16.8	70.0	75395	US-10-274-194-3	Sequence 3, Appl
C 33	16.6	69.2	444	US-09-270-767-2199	Sequence 2199, App
C 34	16.6	69.2	444	US-09-270-767-17481	Sequence 17481, App
C 35	16.6	69.2	539	US-09-513-999C-10940	Sequence 10940, App
C 36	16.6	69.2	1776	US-09-489-039A-3634	Sequence 3634, App
C 37	16.6	69.2	4371	US-08-803-972-1	Sequence 1, Appl
C 38	16.6	69.2	4371	US-08-803-972-1	Sequence 1, Appl
C 39	16.4	68.3	168174	US-10-071-411A-63	Sequence 63, Appl
C 40	16.4	68.3	168273	US-10-071-411A-2	Sequence 2, Appl
C 41	16.2	67.5	336	US-09-513-999C-24032	Sequence 24032, App
C 42	16.2	67.5	627	US-09-270-767-12248	Sequence 12248, App
C 43	16.2	67.5	4792	US-08-781-891-205	Sequence 205, App
C 44	16.2	67.5	4792	US-09-618-166-205	Sequence 205, App
C 45	16.2	67.5	6476	US-09-127-670-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-629-600-18/c
Sequence 18, Application US/08629600
Patent No. 5783196
GENERAL INFORMATION:
APPLICANT: NORIEGA, Fernando
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-629-600-18
Query Match 100.0% ; Score 24 ; DB 1 ; Length 43 ;
Best Local Similarity 100.0% ; Pred. No. 0.029 ;
Matches 24 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Qy 1 TGCACAGACTGCGTCAGTGAGGT 24
Db 37 TGCACAGACTGCGTCAGTGAGGT 14

Fri Feb 11 08:08:37 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:48 ; Search time 673.402 Seconds
(without alignments)
1615.176 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23
Sequence: 1 agcagaagccttacgcttcagc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb da: *
2: gb htg: *
3: gb ln: *
4: gb om: *
5: gb ov: *
6: gb pat: *
7: gb ph: *
8: gb pl: *
9: gb pr: *
10: gb ro: *
11: gb sts: *
12: gb sy: *
13: gb un: *
14: gb vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	6	AX106740 Sequence
2	23	100.0	954	6	AR099864 Sequence
3	23	100.0	954	6	AR431398 Sequence
4	23	100.0	963	1	CFSLTICA
5	23	100.0	981	6	AR099878 Sequence
6	23	100.0	981	6	AR431412 Sequence
7	23	100.0	990	6	AR099887 Sequence
8	23	100.0	990	6	AR431421 Sequence
9	23	100.0	1220	1	AB048835 Escherich
10	23	100.0	1220	1	AB048836 Escherich
11	23	100.0	1220	1	AB048837 Escherich
12	23	100.0	1224	1	AB048239 Escherich
13	23	100.0	1235	6	AR099867 Sequence
14	23	100.0	1235	6	AR431401 Sequence
15	23	100.0	1237	1	AB048240 Escherich
16	23	100.0	1241	1	AB048233 Escherich
17	23	100.0	1241	6	E03959
18	23	100.0	1241	6	E03962
19	23	100.0	1241	7	AY633453

20	23	100.0	1241	7	AY633454 Bacteriop
21	23	100.0	1241	7	AY633455 Bacteriop
22	23	100.0	1241	7	AY633456 Bacteriop
23	23	100.0	1241	7	AY633457 Bacteriop
24	23	100.0	1241	7	AY633458 Bacteriop
25	23	100.0	1241	7	AY633459 Bacteriop
26	23	100.0	1241	7	AY633460 Bacteriop
27	23	100.0	1241	7	AY633461 Bacteriop
28	23	100.0	1241	7	AY633462 Bacteriop
29	23	100.0	1241	7	AY633463 Bacteriop
30	23	100.0	1241	7	AY633464 Bacteriop
31	23	100.0	1241	7	AY633465 Bacteriop
32	23	100.0	1241	7	AY633466 Bacteriop
33	23	100.0	1241	7	AY633467 Bacteriop
34	23	100.0	1241	7	AY633468 Bacteriop
35	23	100.0	1241	7	AY633469 Bacteriop
36	23	100.0	1241	7	AY633470 Bacteriop
37	23	100.0	1241	7	AY633471 Bacteriop
38	23	100.0	1241	7	AY633472 Bacteriop
39	23	100.0	1241	7	AY633473 Bacteriop
40	23	100.0	1242	6	E30432 Method for
41	23	100.0	1254	1	AB015057 Escherich
42	23	100.0	1254	1	AB030484 Escherich
43	23	100.0	1254	6	AR433378 Sequence
44	23	100.0	1254	6	AX139386 Sequence
45	23	100.0	1254	6	BD010259 Nucleic a

ALIGNMENTS

RESULT 1
AX106740 Sequence 8 from Patent WO0123607.
AX106740
AX106740.1 GI:13922401

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Gunzer, F. and Bellin, T.
Multiplex PCR for detecting ehc infections
Patent: WO 0123607-A 8 05-APR-2001;
Roche Diagnostics GmbH (DE)
Location/Qualifiers

1..23
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"

ORIGIN

Query Match 100.0%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAAGCCTTACGCTTCAGGC 23
|||||
1 AGCAGAAGCCTTACGCTTCAGGC 23

Db 1 AGCAGAAGCCTTACGCTTCAGGC 23

RESULT 2
AR099864 Sequence 5 from patent US 6060400.
AR099864
AR099864.1 GI:12810312

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

954 bp DNA linear PAT 14-FEB-2001
Unknown.
Unknown.
Unclassified.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:54:43 ; Search time 177.005 Seconds
(without alignments)
682.108 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcgaagcctacgtcagcgc 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	5	AAF61485
2	23	100.0	282	12	ADN02038
3	23	100.0	954	2	AAAT42651
4	23	100.0	954	3	AAAS1196
5	23	100.0	954	6	ABK11777
6	23	100.0	980	2	AAAT42665
7	23	100.0	981	3	AAAS1210
8	23	100.0	981	6	ABK11791
9	23	100.0	989	3	AAAT42674
10	23	100.0	990	3	AAAS1219
11	23	100.0	990	6	ABK11800
12	23	100.0	1201	6	AAV11405
13	23	100.0	1217	2	AAV11406
14	23	100.0	1232	11	ADL25585
15	23	100.0	1232	11	ADL25580
16	23	100.0	1232	11	ADL25578
17	23	100.0	1234	11	ADL25581
18	23	100.0	1235	2	AAAT42654
19	23	100.0	1235	3	AAAS1199
20	23	100.0	1235	6	ABK11780
21	23	100.0	1242	3	AAZ44676

22	23	100.0	1254	4	AAAC91779
23	23	100.0	1254	10	ADH22653
24	23	100.0	1259	4	AAH01086
25	23	100.0	1479	2	AAV11401
26	23	100.0	1612	8	ACR64707
27	23	100.0	1612	10	ADP43307
28	23	100.0	1664	2	AAZ27688
29	23	100.0	2085	3	AAAS1227
30	23	100.0	2085	6	ABK11958
31	23	100.0	2135	2	AAAT42672
32	23	100.0	2136	3	AAAS1217
33	23	100.0	2136	6	ABK11798
34	23	100.0	61663	9	ACD19049
35	23	100.0	62708	10	ADCC0019
36	23	100.0	134141	6	ABN83487
37	23	93.0	960	10	ADH34345
38	21.4	93.0	960	10	ADH34301
39	21.4	93.0	960	10	ADH34343
40	21.4	93.0	1234	11	ADL25582
41	21.4	93.0	1235	11	ADL25584
42	21.4	93.0	1235	11	ADL25583
43	19.8	86.1	960	10	ADH34339
44	19.8	86.1	960	10	ADH34337
45	18.4	80.0	576	10	ADD33754

ALIGNMENTS

RESULT 1
AAF61485
ID AAF61485 standard; DNA; 23 BP.

AC AAF61485;
DT 18-JUN-2001 (first entry)
DE EHEC pig pathogen strx2 probe SEQ ID 8.
XX EHEC infection; multiplex amplification; detection; human; pig;
KW enterohemorrhagic Escherichia coli infection; pathogen; probe; ss.
XX Escherichia coli.
OS
PN DB19946296-Al.
PD 29-MAR-2001.
XX
XX 28-SEP-1999; 99DE-01046296.
PF 28-SEP-1999; 99DE-01046296.
XX
PR 28-SEP-1999; 99DE-01046296.
XX
XX (HOF) ROCHE DIAGNOSTICS GMBH.
PA
PI Gunzer F, Bellin T;
XX WPI; 2001-246145/26.
DR
XX
XX
PT Primers for amplifying Shiga toxin sequences in Escherichia coli, useful
in multiplex amplification detection of enterohemorrhagic strains.
PS Claim 11; Page 11; 14pp; German.
XX
XX This invention describes a novel primer (P1) which can be used in a
multiplex amplification reaction for detecting clinically important EHEC
(enterohemorrhagic Escherichia coli) infections. P1 allow simultaneous
detection of human and pig pathogens in a single measurement
XX
SQ Sequence 23 BP; 6 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52 ; Search time 45.4639 Seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 28
Sequence: 1 agagcagcttcgcttgcactgtca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/ackfilseq1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	28	100.0	954	3	US-08-816-977-5
2	28	100.0	954	4	US-09-334-477-5
3	28	100.0	981	3	US-08-816-977-24
4	28	100.0	981	4	US-09-334-477-24
5	28	100.0	990	3	US-08-816-977-38
6	28	100.0	990	4	US-09-334-477-38
7	28	100.0	1235	3	US-08-816-977-10
8	28	100.0	1235	4	US-09-334-477-10
9	28	100.0	1254	4	US-09-599-0324-3
10	28	100.0	2085	3	US-08-816-977-48
11	28	100.0	2085	4	US-09-334-477-48
12	28	100.0	2136	3	US-08-816-977-34
13	28	100.0	2136	4	US-09-334-477-34
14	28	100.0	61663	3	US-09-453-7028-62
15	19.6	70.0	1038	4	US-09-248-796A-11678
16	18.2	65.0	2406	4	US-09-543-681A-3189
17	17.8	63.6	327	4	US-09-248-796A-11059
18	17.8	63.6	582	4	US-09-621-976-16905
19	17.4	62.1	582	4	US-09-976-594-516
20	17.4	62.1	2483	2	US-08-177-109A-1
21	17.4	62.1	2483	2	US-08-687-706-1
22	17.4	62.1	2505	4	US-09-799-451-179
23	17.4	62.1	2733	4	US-09-976-594-517
24	17.2	61.4	74	4	US-09-508-930D-45
25	17.2	61.4	810	4	US-09-543-681A-2228
26	17	60.7	846	3	US-09-134-001C-1012
27	17	60.7	1767	4	US-09-601-198-72

28	17	60.7	4832	4	US-08-956-171E-189	Sequence 189, App
29	17	60.7	4832	4	US-08-781-986A-189	Sequence 189, App
30	17	60.7	7070	1	US-08-619-554-3	Sequence 3, Appl1
31	17	60.7	12685	4	US-09-479-467A-3	Sequence 3, Appl1
32	16.8	60.0	168	2	US-08-447-173A-53	Sequence 53, Appl
33	16.8	60.0	235	4	US-09-513-999C-26560	Sequence 26560, A
34	16.8	60.0	238	4	US-09-270-767-7511	Sequence 7511, Ap
35	16.8	60.0	238	4	US-09-270-767-22793	Sequence 22793, A
36	16.8	60.0	420	4	US-09-513-999C-28267	Sequence 28267, A
37	16.8	60.0	558	4	US-09-248-796A-10214	Sequence 10214, A
38	16.8	60.0	670	3	US-09-306-446C-15	Sequence 15, Appl
39	16.8	60.0	779	1	US-08-592-214A-9	Sequence 9, Appl1
40	16.8	60.0	779	3	US-08-659-188-9	Sequence 9, Appl1
41	16.8	60.0	779	3	US-08-655-227-9	Sequence 9, Appl1
42	16.8	60.0	779	3	US-08-655-241-9	Sequence 9, Appl1
43	16.8	60.0	779	3	US-09-149-976-9	Sequence 9, Appl1
44	16.8	60.0	779	3	US-09-398-326-9	Sequence 9, Appl1
45	16.8	60.0	1541	4	US-09-518-914-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-816-977-5
Sequence 5, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kaitlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..954
US-08-816-977-5
Query Match 100.0%; Score 28; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 / Search time 1927.24 Seconds
(Without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-7

Perfect score: 1 agagcagcttcgtcgttcgtcactgca 28

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

BST: *
1: gb_satl.*
2: gb_satl2.*
3: gb_hlc.*
4: gb_satl3.*
5: gb_satl4.*
6: gb_satl5.*
7: gb_satl6.*
8: gb_satl7.*
9: gb_satl8.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	73.6	635	BZ887470	BZ887470 CH240.198
2	20.6	73.6	770	BZ775723	BZ775723 ih95607.9
3	20.6	73.6	806	BZ159158	BZ159158 CH230-376
4	20.6	73.6	897	CB197911	CB197911 AGENCOURT
5	20.6	73.6	962	CC735187	CC735187 OGVB82TH
6	20.6	73.6	1468	CN505340	AL138993 Tetradon
7	20.2	72.1	858	A1422096	A1422096 tef57h05.x
8	20.2	71.4	828	BZ342868	BZ342868 8004. Rabd
9	20.2	71.4	527	AL837591	AL837591 AL837591
10	20.2	71.4	829	CC578661	CC578661 CH240.457
11	20.2	71.4	815	BI737664	BI737664 603358577
12	20.2	71.4	822	BI550495	BI550495 603195417
13	20.2	71.4	893	BUI32590	BUI32590 60312189
14	20.2	71.4	1225	BGI15160	BGI15160 603316031
15	19.8	70.7	450	R42075	R42075 yf98601.81
16	19.8	70.7	631	BUI221953	BUI221953 603754843
17	19.8	70.7	729	BUI258365	BUI258365 603742872
18	19.8	70.7	1144	CL052971	CL052971 CH216-76N
19	19.6	70.0	478	AC431086	AC431086 HS.5087.A
20	19.6	70.0	605	CF112629	CF112629 Shltzomi
21	19.6	70.0	627	AC421708	AC421708 IM020005
22	19.6	70.0	726	AQ840728	AQ840728 nbxb0068L
23	19.6	70.0	779	BH073448	BH073448 RPCI-24-2
24	19.6	70.0	802	CF289530	CF289530 AGENCOURT

C 25	19.6	70.0	1147	2	BF039006	BF039006 601461336
C 26	19.4	69.3	372	7	CO219380	CO219380 WS0107.B2
C 27	19.4	69.3	372	7	CO219417	CO219417 WS0107.B2
C 28	19.2	68.6	226	9	CE657761	CE657761 tigr-gss-
C 29	19.2	68.6	375	5	BI447986	BI447986 BY447986
C 30	19.2	68.6	467	9	CE659430	CE659430 tigr-gss-
C 31	19.2	68.6	487	9	CE542794	CE542794 tigr-gss-
C 32	19.2	68.6	522	9	CE069480	CE069480 tigr-gss-
C 33	19.2	68.6	522	9	CE447512	CE447512 tigr-gss-
C 34	19.2	68.6	574	9	CE332237	CE332237 tigr-gss-
C 35	19.2	68.6	584	9	CE342207	CE342207 tigr-gss-
C 36	19.2	68.6	618	9	CE277455	CE277455 tigr-gss-
C 37	19.2	68.6	628	9	CE573420	CE573420 tigr-gss-
C 38	19.2	68.6	686	1	AU005087	AU005087 AU005087
C 39	19.2	68.6	703	9	CE133005	CE133005 tigr-gss-
C 40	19.2	68.6	707	9	BQ898634	BQ898634 AGENCOURT
C 41	19.2	68.6	957	5	CL034070	CL034070 CH216-37G
C 42	19.2	68.6	1023	9	AM892893	AM892893 CM2-NN00
C 43	19.2	67.9	289	8	BZ155702	BZ155702 CH230-300
C 44	19.2	67.9	350	8	BZ155702	BZ155702 CH230-300
C 45	19.2	67.9	403	7	T95154	T95154 y639d05.r1

ALIGNMENTS

RESULT 1
BZ887470
LOCUS
DEFINITION
CH240.198C16.TJ CHORI-240 Bos taurus genomic clone CH240.198C16.
genomic survey sequence.
ACCESSION
BZ887470
VERSION
BZ887470.1 GI:29114872
KEYWORDS
GSS.
SOURCE
Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 635)
Zhao,S., Shetty,J., Shatsman,S., Tsagaye,G., Geer,K., Shvartbeyn,A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P., Crawford,A.M. and McMan,J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org

TITLE
JOURNAL
COMMENT
Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdjong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by AGRsearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.
Plate: 198 row: C column: 16
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..635
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_198C16"
/sex="Male"
/cell_type="blood"
/clone_lib="CHORI-240"

FEATURES
source

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1593.09 Seconds

(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-8

Perfect score: 23

Sequence: 1 agcgaagcctcagctcagc 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.8	86.1	632	2	BB608995
2	19.8	86.1	2148	3	AK054278
3	19.4	84.3	590	5	BQ121748
4	19.4	84.3	596	4	BG592107
5	19.4	84.3	597	5	BQ121747
6	18.8	81.7	303	5	BY032941
7	18.4	80.0	346	5	CG69077
8	18.4	80.0	356	5	BY136877
9	18.4	80.0	361	5	BY133551
10	18.4	80.0	380	5	CC200394
11	18.4	80.0	381	9	CG561824
12	18.4	80.0	392	1	AI930332
13	18.4	80.0	400	5	BY075663
14	18.4	80.0	419	5	BY033588
15	18.4	80.0	422	5	BY227863
16	18.4	80.0	424	5	CG523885
17	18.4	80.0	427	7	W83819
18	18.4	80.0	437	5	BY252038
19	18.4	80.0	447	9	CG574608
20	18.4	80.0	452	2	BB137544
21	18.4	80.0	454	2	CG610742
22	18.4	80.0	468	6	CP160973
23	18.4	80.0	474	4	BG971552

25	18.4	80.0	479	1	AI116569
26	18.4	80.0	483	4	BG061488
27	18.4	80.0	494	6	CA886486
28	18.4	80.0	498	1	AA914041
29	18.4	80.0	501	5	BX521078
30	18.4	80.0	505	9	CG654782
31	18.4	80.0	508	6	CA884326
32	18.4	80.0	512	7	CA884326
33	18.4	80.0	513	7	CA884326
34	18.4	80.0	517	9	CG604615
35	18.4	80.0	520	1	AI1255684
36	18.4	80.0	522	1	AI1255684
37	18.4	80.0	523	6	CP166500
38	18.4	80.0	529	2	BE370517
39	18.4	80.0	533	2	AM611168
40	18.4	80.0	537	2	AM012317
41	18.4	80.0	546	2	BE134721
42	18.4	80.0	548	6	CA551676
43	18.4	80.0	549	2	AM012224
44	18.4	80.0	561	2	BF100103
45	18.4	80.0	570	2	AM412918

ALIGNMENTS

RESULT 1
LOCUS BB608995/c
DEFINITION BB608995 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E33009J08 5', mRNA sequence.
ACCESSION BB608995
VERSION BB608995.2 GI:16451136
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 632)
AUTHORS Aikawa, T., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Aikawa, T., et al. 2001)
Unpublished (2001)

TITLE JOURNAL
COMMENT On Dec 6, 2000 this sequence version replaced GI:11564171.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waghi, K., Fujiwara, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E., Matsushita, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1651.92 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-6

Perfect score: 24

Sequence: 1.tgccacagctgcgtcagtcagagct 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	164	4	BG384763
2	19.8	82.5	864	8	BZ137613
3	19.2	80.0	319	6	BY794428
4	19.2	80.0	331	5	BY145728
5	19.2	80.0	366	5	BY168177
6	19.2	80.0	380	2	BB842411
7	19.2	80.0	462	2	BB842411
8	19.2	80.0	483	6	CB545045
9	19.2	80.0	573	6	AO570333
10	19.2	80.0	697	9	CR022070
11	19.2	80.0	717	2	BES69949
12	19.2	80.0	865	6	CB13571
13	19.2	80.0	866	4	BI659266
14	19.2	80.0	1262	6	CA492803
15	19.2	80.0	3022	3	AK004595
16	19.2	80.0	3124	3	BC027329
17	19.2	80.0	3214	3	BC048910
18	18.8	78.3	711	9	AG335488
19	18.8	78.3	749	9	AG442797
20	18.8	78.3	753	9	CE321712
21	18.2	75.8	385	6	BY647886
22	18.2	75.8	424	8	AO681986
23	18.2	75.8	450	1	AU062893
24	18.2	75.8	480	2	BF603001

25	18.2	75.8	520	7	AK107635	CK107635
26	18.2	75.8	563	8	AA0122468	AA0122468
27	18.2	75.8	624	8	AZ759334	AZ759334
28	18.2	75.8	680	8	BZ737939	BZ737939
29	18.2	75.8	758	9	CC726778	CC726778
30	18.2	75.8	765	9	CC708643	CC708643
31	18.2	75.8	789	8	BZ737943	BZ737943
32	18.2	75.8	791	6	CD647854	CD647854
33	18.2	75.8	856	9	CNS05851	CNS05851
34	18.2	75.8	857	5	B0205885	B0205885
35	18.2	75.8	904	5	B0222225	B0222225
36	18.2	75.8	1011	9	CG348401	CG348401
37	18.2	75.8	1020	9	CL209120	CL209120
38	17.8	74.2	190	4	BG305521	BG305521
39	17.8	74.2	191	8	AZ251801	AZ251801
40	17.8	74.2	260	7	CN168920	CN168920
41	17.8	74.2	373	2	AW154327	AW154327
42	17.8	74.2	437	6	CA951575	CA951575
43	17.8	74.2	495	8	AZ878920	AZ878920
44	17.8	74.2	512	8	AQ933350	AQ933350
45	17.8	74.2	522	7	CK383349	CK383349

ALIGNMENTS

RESULT 1
BG384763
LOCUS: BG384763 164 bp mRNA linear EST 12-MAR-2001
DEFINITION: 304043 MARC 1PTG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION: BG384763
VERSION: BG384763.1 GI:13309235
KEYWORDS: EST.
SOURCE: Sus scrofa (pig)
ORGANISM: Sus scrofa

REFERENCE: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus. 1 (bases 1 to 164)
AUTHORS: Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Perce, G., Sultana, R., Quackenbush, J., and Keel, J.W.
TITLE: Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
JOURNAL: Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE: 22213789
PUBMED: 12226715

COMMENT: Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@ma.ars.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 92 row: P column: 18
Seq primer: ATTAGGTGACATATG.
Location/Qualifiers
1. 164
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/feature_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 1PTG"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1445.43 Seconds

(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 21

Sequence: 1 cgatattccggaagacacattg 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est1:*
9: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	87.6	481	9	CC880516
C 2	18.4	87.6	799	9	CC830906
C 3	17.8	84.8	302	5	BQ37313
C 4	17.4	82.9	740	9	CL196951
C 5	17.4	82.9	844	2	BP796995
C 6	17	81.0	443	2	AM872041
C 7	17	81.0	543	4	B0613139
C 8	17	81.0	554	4	B1442079
C 9	17	81.0	689	6	CB593139
C 10	17	81.0	720	5	BP726595
C 11	17	81.0	758	5	BP723599
C 12	17	81.0	760	7	BP688365
C 13	17	81.0	762	7	BP692248
C 14	17	81.0	809	6	CA789606
C 15	17	81.0	812	6	CD360247
C 16	17	81.0	826	6	CD301144
C 17	17	81.0	852	6	CD361666
C 18	17	81.0	852	6	CD361666
C 19	17	81.0	877	6	CB196834
C 20	17	81.0	927	6	CD302134
C 21	16.8	80.0	933	6	CA973359
C 22	16.8	80.0	201	6	CD183502
C 23	16.8	80.0	371	7	CF501009
C 24	16.8	80.0	380	6	CD186770
			391	9	CG416831
					CG416831 ZMMBBc002

25	16.8	80.0	393	9	CG416853
26	16.8	80.0	438	9	AG194060
27	16.8	80.0	442	2	BP858265
28	16.8	80.0	453	1	AV736811
C 29	16.8	80.0	472	6	CD163413
C 30	16.8	80.0	477	7	CF503348
C 31	16.8	80.0	481	8	AQ507070
C 32	16.8	80.0	550	8	BH081823
C 33	16.8	80.0	559	8	BH203322
C 34	16.8	80.0	668	9	CG866976
C 35	16.8	80.0	690	7	CF500020
C 36	16.8	80.0	694	8	CC175967
C 37	16.8	80.0	695	3	AY432489
C 38	16.8	80.0	723	7	CN038101
C 39	16.8	80.0	729	2	BF793256
C 40	16.8	80.0	777	7	CG200402
C 41	16.8	80.0	778	9	CG703102
C 42	16.8	80.0	815	2	BE793728
C 43	16.8	80.0	918	4	BG388642
C 44	16.8	80.0	1037	9	CG423348
C 45	16.8	80.0	1044	9	CG685298

ALIGNMENTS

RESULT 1
CC880516/c
LOCUS ZMMBBb0218A02.f ZMMBBb Zea mays genomic clone ZMMBBb0218A02 5'
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 481)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wing, R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0218 row: A column: 02
Seq primer: T7
Class: BAC ends.

FEATURES

source
location/Qualifiers
1..481
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0218A02"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/note="Vector: pBeloBAC11, Site 1: HindIII, Site 2:
HindIII; Zea mays l. ssp. mays" -

ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 481;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1651.92 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-2

Perfect score: 24

Sequence: 1 ccggacacatagaagaactcat 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20.8	86.7	949	3	CR670603 Tetraodon
C 2	19.8	82.5	680	7	CN326151 AGENCOURT
C 3	19.2	80.0	156	2	AW885334 QV4-OT006
C 4	19.2	80.0	763	9	CNS049GR
C 5	19.2	80.0	805	9	CE323459
C 6	19.2	80.0	940	9	CNS04HJ
C 7	18.8	78.3	483	4	BI138333
C 8	18.8	78.3	528	4	CKO91504
C 9	18.8	78.3	530	7	CK101628
C 10	18.4	76.7	618	5	BP724915
C 11	18.4	76.7	452	7	CN938218
C 12	18.4	76.7	579	8	BH320282
C 13	18.4	76.7	914	8	BZ236055
C 14	18.2	75.8	101	8	AQ286508
C 15	18.2	75.8	114	7	CR434085
C 16	18.2	75.8	308	1	AL962135
C 17	18.2	75.8	311	1	AL955012
C 18	18.2	75.8	347	5	BP675436
C 19	18.2	75.8	360	1	AU245212
C 20	18.2	75.8	360	1	AU245214
C 21	18.2	75.8	375	1	AU244699
C 22	18.2	75.8	381	4	BU096785
C 23	18.2	75.8	387	7	CF786403
C 24	18.2	75.8	392	1	AL644866

C 25	18.2	75.8	401	1	AL875276
C 26	18.2	75.8	406	8	CC057478
C 27	18.2	75.8	408	7	CN109513
C 28	18.2	75.8	409	1	AL787946
C 29	18.2	75.8	414	1	AL794318
C 30	18.2	75.8	429	7	CN119667
C 31	18.2	75.8	436	1	AL774003
C 32	18.2	75.8	445	1	AL968405
C 33	18.2	75.8	456	7	CN119519
C 34	18.2	75.8	458	7	CN114585
C 35	18.2	75.8	467	1	AL970785
C 36	18.2	75.8	477	1	AL791399
C 37	18.2	75.8	482	1	AL777926
C 38	18.2	75.8	484	4	BU611732
C 39	18.2	75.8	486	2	AL791571
C 40	18.2	75.8	492	2	AW147738
C 41	18.2	75.8	507	4	BG553712
C 42	18.2	75.8	510	7	CN119608
C 43	18.2	75.8	512	4	BU633081
C 44	18.2	75.8	513	1	AL673077
C 45	18.2	75.8	513	4	BG162432

ALIGNMENTS

RESULT 1
LOCUS CR670603/c 949 bp mRNA linear HTC 11-AUG-2004
DEFINITION Tetraodon nigroviridis full-length cDNA.
ACCESSION CR670603
VERSION CR670603.1 GI:51167048
KEYWORDS HTC; cDNA; full-length; Tetraodon nigroviridis.
SOURCE Tetraodon
ORGANISM Tetraodon
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae.
1 (bases 1 to 949)
Genoscope.
Direct Submission
Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
(E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES

source
Location/Qualifiers
1..949
/organism="Tetraodon"
/mol_type="mRNA"
/db_xref="taxon:47144"
/tissue_type="muscle"

Query Match 86.7%; Score 20.8; DB 3; Length 949;
Best Local Similarity 91.7%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
1 CCGGACATATGAAAGAAATCTCAT 24
|||||
24 CCGGCACACAGGAAGAAATCTCAT 1

RESULT 2

LOCUS CN326151 680 bp mRNA linear EST 14-APR-2004
DEFINITION AGENCOURT 22000357 NICHD XGC Te2 Xenopus laevis cDNA clone
ACCESSION CN326151
VERSION CN326151.1 GI:46383787
KEYWORDS EST.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:59:52; Search time 38.9691 seconds
(without alignments)
437.756 Million cell updates/sec

Title: US-10-089-487-2
Perfect score: 24
Sequence: 1 ccgacacatagaagaactcat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	100.0	945 3 US-08-816-977-1	Sequence 1, Appl
2	24	100.0	945 4 US-09-334-477-1	Sequence 1, Appl
3	24	100.0	969 3 US-08-816-977-20	Sequence 20, Appl
4	24	100.0	969 4 US-09-334-477-20	Sequence 20, Appl
5	24	100.0	981 3 US-08-816-977-36	Sequence 36, Appl
6	24	100.0	981 4 US-09-334-477-36	Sequence 36, Appl
7	24	100.0	1241 3 US-08-816-977-9	Sequence 9, Appl
8	24	100.0	1241 4 US-09-334-477-9	Sequence 9, Appl
9	24	100.0	2073 3 US-08-816-977-46	Sequence 46, Appl
10	24	100.0	2073 4 US-09-334-477-46	Sequence 46, Appl
11	24	100.0	2127 3 US-08-816-977-32	Sequence 32, Appl
12	24	100.0	2127 4 US-09-334-477-32	Sequence 32, Appl
13	24	100.0	48908 3 US-09-453-7028-137	Sequence 137, App
14	19	79.2	70 1 US-07-488-430-75	Sequence 75, Appl
15	19	79.2	70 1 US-08-425-336-73	Sequence 73, Appl
16	19	79.2	70 1 US-08-488-113B-73	Sequence 73, Appl
17	19	79.2	70 1 US-08-477-484B-73	Sequence 73, Appl
18	19	79.2	70 2 US-08-646-360-73	Sequence 73, Appl
19	19	79.2	70 3 US-08-839-765-73	Sequence 73, Appl
20	19	79.2	70 3 US-09-136-389-73	Sequence 73, Appl
21	19	79.2	70 3 US-09-610-838-73	Sequence 73, Appl
22	19	79.2	70 4 US-09-711-485-73	Sequence 73, Appl
23	19	79.2	70 5 PCT-US92-09487-75	Sequence 75, Appl
24	19	79.2	78 1 US-07-988-430-76	Sequence 76, Appl
25	19	79.2	78 1 US-08-425-336-74	Sequence 74, Appl
26	19	79.2	78 1 US-08-488-113B-74	Sequence 74, Appl
27	19	79.2	78 1 US-08-477-484B-74	Sequence 74, Appl

28	19	79.2	78 2 US-08-646-360-74	Sequence 74, Appl
29	19	79.2	78 3 US-08-839-765-74	Sequence 74, Appl
30	19	79.2	78 3 US-09-136-389-74	Sequence 74, Appl
31	19	79.2	78 3 US-09-610-838-74	Sequence 74, Appl
32	19	79.2	78 3 US-09-711-485-74	Sequence 74, Appl
33	19	79.2	78 5 PCT-US92-09487-76	Sequence 76, Appl
34	19	79.2	78 5 US-08-621-803-250	Sequence 250, App
35	19	79.2	78 2 US-08-621-803-250	Sequence 250, App
36	17.2	71.7	2484 2 US-09-377-497-68	Sequence 68, Appl
37	16.8	70.0	513 4 US-09-621-976-3864	Sequence 3864, Ap
38	16.6	69.2	1989 4 US-09-534-228B-6	Sequence 6, Appl
39	16.6	69.2	903 4 US-09-134-000C-230	Sequence 230, App
40	16.6	69.2	2151 4 US-08-916-421B-1	Sequence 11481, A
41	16.6	69.2	1664976 4 US-08-916-421B-1	Sequence 1, Appl
42	16.6	69.2	1664976 4 US-09-270-767-11481	Sequence 1, Appl
43	16.4	68.3	32768 4 US-09-692-570-1	Sequence 71, Appl
44	16.2	67.5	363 4 US-08-961-527-71	Sequence 17385, A
45	16.2	67.5	441 4 US-09-621-976-9317	Sequence 9317, Ap

ALIGNMENTS

RESULT 1
US-08-816-977-1/c
Sequence 1, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPND-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..945
US-08-816-977-1
Query Match 100.0%; Score 24; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1651.92 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-1

Perfect score: 24
Sequence: 1 agtgcgcagggagtcagataat 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	164	4	BG384763 304043 MA
C 2	19.8	82.5	427	8	BH172878 SALK 0063
C 3	18.2	75.8	411	1	AL783578 AL783578
C 4	18.2	75.8	615	5	BX909957 BX909957
C 5	18.2	75.8	728	5	BX864637 BX864637
C 6	18.2	75.8	803	9	AG283545 AG283545
C 7	18.2	75.8	975	8	AQ446367 nxb00069B
C 8	17.8	74.2	267	8	BB002225 BB002225
C 9	17.6	73.3	160	7	CF497459 MS1-0081G
C 10	17.6	73.3	298	7	CF502432 CF502432
C 11	17.6	73.3	327	7	CF502432 MS1-0046T
C 12	17.6	73.3	343	2	BB793708 BB793708
C 13	17.6	73.3	363	2	BB791897 BB791897
C 14	17.6	73.3	367	2	BB791897 BB791897
C 15	17.6	73.3	388	2	BB790895 BB790895
C 16	17.6	73.3	396	7	CF498103 MS1-0055G
C 17	17.6	73.3	401	7	CF500042 MS1-0030T
C 18	17.6	73.3	403	7	CF500173 MS1-0062P
C 19	17.6	73.3	403	7	CF500266 MS1-0014T
C 20	17.6	73.3	403	7	CF502313 MS1-0014T
C 21	17.6	73.3	420	2	BB780379 BB780379
C 22	17.6	73.3	420	2	CF503515 MS1-0055G
C 23	17.6	73.3	442	7	CF502392 MS1-0082U
C 24	17.6	73.3	444	7	CF502893 MS1-0131U

25	17.6	73.3	451	7	CP499126
C 26	17.6	73.3	453	7	CF500859
C 27	17.6	73.3	460	7	CF500597 MS1-0128T
C 28	17.6	73.3	466	7	CF503798 MS1-0131U
C 29	17.6	73.3	476	6	CD808925
C 30	17.6	73.3	481	7	CP498432
C 31	17.6	73.3	500	5	BU832097
C 32	17.6	73.3	534	1	AI977736
C 33	17.6	73.3	558	4	CF498100
C 34	17.6	73.3	588	4	BU123197
C 35	17.6	73.3	592	7	CF500084
C 36	17.6	73.3	608	7	CF500290
C 37	17.6	73.3	639	7	CF501970
C 38	17.6	73.3	640	4	BM398010
C 39	17.6	73.3	658	5	BX505023
C 40	17.6	73.3	658	9	BX963969
C 41	17.6	73.3	710	9	CC526941
C 42	17.6	73.3	801	6	CD756146
C 43	17.6	73.3	807	9	CC780686
C 44	17.6	73.3	897	2	BF127421
C 45	17.6	73.3	897	7	CK629187

ALIGNMENTS

RESULT 1
LOCUS BG384763 164 bp mRNA linear EST 12-MAR-2001
DEFINITION BG384763 304043 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG384763
VERSION BG384763.1 GI:13309235
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 164)
Fahrentkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J., and Keefe, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL
MEDLINE
PubMed
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@ma.ars.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.98004.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 92 row: P column: 18
Seq primer: ATTAGTACACCTATAG.
Location/Qualifiers
1..164

FEATURES
source
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 04:57:52 ; Search time 1376.6 Seconds
(without alignments)
529.417 Million cell updates/sec

Title: US-10-089-487-3

Perfect score: 20

Sequence: 1 ttccggaatgcataatcagtc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	87.0	181	1	AV112270 AV112270
C 2	17.4	87.0	229	1	AV361260 AV361260
C 3	17.4	87.0	675	8	BH982496 BH982496
C 4	17.4	87.0	910	6	CA472629 CA472629
C 5	16.8	84.0	203	9	CE577268 CE577268
C 6	16.8	84.0	229	9	CO371015 CO371015
C 7	16.8	84.0	234	2	BH166371 BH166371
C 8	16.8	84.0	253	2	BH221661 BH221661
C 9	16.8	84.0	292	5	BQ626804 BQ626804
C 10	16.8	84.0	340	7	CO746789 CO746789
C 11	16.8	84.0	417	5	BU429239 BU429239
C 12	16.8	84.0	456	5	BQ482167 BQ482167
C 13	16.8	84.0	480	2	AW547090 AW547090
C 14	16.8	84.0	485	5	BQ482333 BQ482333
C 15	16.8	84.0	485	5	BQ482335 BQ482335
C 16	16.8	84.0	490	5	BQ482064 BQ482064
C 17	16.8	84.0	490	5	BQ482530 BQ482530
C 18	16.8	84.0	502	5	BQ482357 BQ482357
C 19	16.8	84.0	513	5	BQ482145 BQ482145
C 20	16.8	84.0	579	7	CN775343 CN775343
C 21	16.8	84.0	586	7	CO371014 CO371014
C 22	16.8	84.0	597	7	CO371002 CO371002
C 23	16.8	84.0	621	5	BX505754 BX505754
C 24	16.8	84.0	653	8	AZ358338 AZ358338

C 25	16.8	84.0	663	9	CE507740 CE507740
C 26	16.8	84.0	759	9	AG478858 AG478858
C 27	16.8	84.0	785	2	BF862749 BF862749
C 28	16.8	84.0	829	9	BG698414 BG698414
C 29	16.8	84.0	902	9	CC549036 CC549036
C 30	16.8	84.0	261	4	BI241119 BI241119
C 31	16.4	82.0	282	4	BI355815 BI355815
C 32	16.4	82.0	294	4	BI243027 BI243027
C 33	16.4	82.0	385	1	AI617042 AI617042
C 34	16.4	82.0	403	1	AA695947 AA695947
C 35	16.4	82.0	414	2	AW771236 AW771236
C 36	16.4	82.0	423	4	BI683805 BI683805
C 37	16.4	82.0	489	1	AA695937 AA695937
C 38	16.4	82.0	489	4	BI430369 BI430369
C 39	16.4	82.0	551	2	BE557055 BE557055
C 40	16.4	82.0	552	5	BO285434 BO285434
C 41	16.4	82.0	574	4	BG892067 BG892067
C 42	16.4	82.0	578	4	BI229069 BI229069
C 43	16.4	82.0	600	5	BU925349 BU925349
C 44	16.4	82.0	609	4	BI242268 BI242268
C 45	16.4	82.0	631	5	BQ449484 BQ449484

ALIGNMENTS

RESULT 1
AV112270/c 181 bp mRNA linear EST 29-JUN-1999
LOCUS AV112270 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
DEFINITION clone 2610010N22, mRNA sequence.
ACCESSION AV112270 GI:5266350
VERSION AV112270.1 GI:5266350

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Mitsuuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagami, K., Yamamura, T., Yokote, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@tc.riken.go.jp

Thermolabile and thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.ttc.riken.go.jp>) for further details.

FEATURES
source
Location/Qualifiers
1..181
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2610010N22"
/sex="mixed"
/dev_stage="10-day embryo"
/clone_lib="Mus musculus C57BL/6J 10-day embryo"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:55:37 ; Search time 170.706 Seconds
(without alignments)
706.850 Million cell updates/sec

Title: US-10-089-487-4

Perfect score: 1 cgatctccggaagacatg 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:
1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/2/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/PCRUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/2/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	100.0	954	9	US-09-334-477-5	Sequence 5, Appl
C 2	100.0	981	9	US-09-334-477-24	Sequence 24, Appl
C 3	100.0	990	9	US-09-334-477-38	Sequence 38, Appl
C 4	100.0	1235	9	US-09-334-477-10	Sequence 10, Appl
C 5	100.0	1612	9	US-09-870-759-27	Sequence 27, Appl
C 6	100.0	1612	10	US-09-751-708A-27	Sequence 27, Appl
C 7	100.0	1612	18	US-10-428-817A-23	Sequence 92, Appl
C 8	100.0	1612	18	US-10-425-821-92	Sequence 92, Appl
C 9	100.0	2085	9	US-09-334-477-48	Sequence 48, Appl
C 10	100.0	2136	9	US-09-334-477-34	Sequence 34, Appl
C 11	100.0	61662	16	US-10-418-837-1	Sequence 1, Appl
C 12	100.0	61663	14	US-10-114-170-62	Sequence 62, Appl

Result No.	Score	Query Match	Length	ID	Description
C 13	16.8	80.0	2624	18	US-10-425-115-78451
C 14	16.8	80.0	5085	17	US-10-437-963-2350
C 15	16.8	80.0	6018	17	US-10-437-963-69454
C 16	16.4	78.1	562	16	US-10-424-599-41130
C 17	16.4	78.1	3411	17	US-10-437-963-78544
C 18	16.4	78.1	160142	13	US-10-027-653-55064
C 19	16.4	78.1	1601042	15	US-10-027-633-55064
C 20	16.4	78.1	4592	14	US-10-193-692-1
C 21	15.8	75.2	223	16	US-10-621-901-85
C 22	15.8	75.2	224	16	US-10-621-901-1858
C 23	15.8	75.2	478	17	US-10-767-701-20241
C 24	15.8	75.2	487	10	US-09-918-995-14811
C 25	15.8	75.2	638	18	US-10-425-115-162587
C 26	15.8	75.2	1272	17	US-10-437-963-23246
C 27	15.8	75.2	1766	16	US-10-412-6998-205
C 28	15.8	75.2	1775	14	US-10-286-264-105
C 29	15.8	75.2	1783	16	US-10-425-114-12995
C 30	15.8	75.2	2046	9	US-09-764-898-95
C 31	15.8	75.2	2492	9	US-09-764-898-95
C 32	15.8	75.2	2971	18	US-10-425-115-22045
C 33	15.8	75.2	4672	13	US-10-194-163-846
C 34	15.8	75.2	4733	17	US-10-437-963-1177
C 35	15.8	75.2	4736	9	US-09-822-830A-35
C 36	15.8	75.2	58965	15	US-10-298-122-2
C 37	15.8	75.2	149480	10	US-09-873-367C-284
C 38	15.8	75.2	149480	10	US-09-873-367C-285
C 39	15.8	75.2	149480	11	US-09-868-007A-222
C 40	15.4	73.3	366	8	US-08-781-986A-4332
C 41	15.4	73.3	366	16	US-10-329-624-4332
C 42	15.4	73.3	582	17	US-10-437-963-64485
C 43	15.4	73.3	594	16	US-10-424-599-73706
C 44	15.4	73.3	732	13	US-10-052-586-577
C 45	15.4	73.3	732	14	US-10-174-590-577

ALIGNMENTS

RESULT 1
US-09-334-477-5/C
Sequence 5, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Veroetoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☒ **BLACK BORDERS**

☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

☐ **FADED TEXT OR DRAWING**

☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**

☐ **SKEWED/SLANTED IMAGES**

☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**

☐ **GRAY SCALE DOCUMENTS**

☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**

☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.